

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:20:03 ; Search time 166 Seconds
(without alignments)
35.086 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRSSVMVHWK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pdb.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pdb.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pdb.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pdb.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pdb.*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pdb.*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pdb.*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*

19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pdb.*

20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdb.*

21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	87	100.0	14	US-09-155-076-1
2	87	100.0	40	US-09-998-042-2
3	87	100.0	44	US-09-155-076-6
4	87	100.0	44	US-09-155-076-8
5	87	100.0	44	US-09-155-076-9
6	87	100.0	53	US-09-155-076-10
7	87	100.0	54	US-09-155-076-7
8	87	100.0	67	US-09-998-042-8
9	87	100.0	614	US-10-116-275-258
10	80	92.0	576	US-10-503-643-3
11	80	92.0	576	US-10-503-691-4

12	78	89.7	27	10	US-09-998-042-3	Sequence 3, Appli
13	65	74.7	574	9	US-09-748-739A-23	Sequence 23, Appli
14	65	74.7	574	14	US-10-032-233-50	Sequence 50, Appli
15	65	74.7	574	16	US-10-413-432-50	Sequence 50, Appli
16	65	74.7	574	16	US-10-324-466-50	Sequence 50, Appli
17	62	71.3	14	9	US-09-155-076-15	Sequence 15, Appli
18	62	71.3	573	18	US-10-728-723-52	Sequence 52, Appli
19	62	71.3	573	18	US-10-728-723-92	Sequence 52, Appli
20	62	71.3	573	18	US-10-728-723-110	Sequence 110, Appli
21	62	71.3	574	9	US-09-748-739A-4	Sequence 4, Appli
22	62	71.3	574	9	US-09-748-739A-6	Sequence 6, Appli
23	62	71.3	574	9	US-09-748-739A-8	Sequence 8, Appli
24	62	71.3	574	9	US-09-748-739A-17	Sequence 17, Appli
25	62	71.3	574	9	US-09-748-739A-18	Sequence 18, Appli
26	62	71.3	574	9	US-09-748-739A-19	Sequence 19, Appli
27	62	71.3	574	9	US-09-748-739A-20	Sequence 20, Appli
28	62	71.3	574	9	US-09-748-739A-21	Sequence 21, Appli
29	62	71.3	574	10	US-09-997-209-89	Sequence 89, Appli
30	62	71.3	574	14	US-10-032-233-2	Sequence 2, Appli
31	62	71.3	574	14	US-10-032-233-4	Sequence 4, Appli
32	62	71.3	574	14	US-10-032-233-6	Sequence 6, Appli
33	62	71.3	574	14	US-10-032-233-8	Sequence 8, Appli
34	62	71.3	574	14	US-10-032-233-10	Sequence 10, Appli
35	62	71.3	574	14	US-10-032-233-12	Sequence 12, Appli
36	62	71.3	574	14	US-10-032-233-14	Sequence 14, Appli
37	62	71.3	574	14	US-10-032-233-16	Sequence 16, Appli
38	62	71.3	574	14	US-10-032-233-18	Sequence 18, Appli
39	62	71.3	574	14	US-10-032-233-20	Sequence 20, Appli
40	62	71.3	574	14	US-10-032-233-22	Sequence 22, Appli
41	62	71.3	574	14	US-10-032-233-24	Sequence 24, Appli
42	62	71.3	574	14	US-10-032-233-26	Sequence 26, Appli
43	62	71.3	574	14	US-10-032-233-28	Sequence 28, Appli
44	62	71.3	574	14	US-10-032-233-30	Sequence 30, Appli
45	62	71.3	574	14	US-10-032-233-32	Sequence 32, Appli
46	62	71.3	574	14	US-10-032-233-34	Sequence 34, Appli
47	62	71.3	574	14	US-10-032-233-36	Sequence 36, Appli
48	62	71.3	574	14	US-10-032-233-38	Sequence 38, Appli
49	62	71.3	574	14	US-10-032-233-40	Sequence 40, Appli
50	62	71.3	574	14	US-10-032-233-42	Sequence 42, Appli
51	62	71.3	574	14	US-10-032-233-44	Sequence 44, Appli
52	62	71.3	574	14	US-10-032-233-46	Sequence 46, Appli
53	62	71.3	574	14	US-10-032-233-48	Sequence 48, Appli
54	62	71.3	574	14	US-10-032-233-50	Sequence 50, Appli
55	62	71.3	574	15	US-10-326-892-2	Sequence 2, Appli
56	62	71.3	574	15	US-10-433-206-89	Sequence 2, Appli
57	62	71.3	574	16	US-10-413-432-2	Sequence 4, Appli
58	62	71.3	574	16	US-10-413-432-4	Sequence 6, Appli
59	62	71.3	574	16	US-10-413-432-6	Sequence 8, Appli
60	62	71.3	574	16	US-10-413-432-8	Sequence 10, Appli
61	62	71.3	574	16	US-10-413-432-10	Sequence 12, Appli
62	62	71.3	574	16	US-10-413-432-12	Sequence 14, Appli
63	62	71.3	574	16	US-10-413-432-14	Sequence 16, Appli
64	62	71.3	574	16	US-10-413-432-16	Sequence 18, Appli
65	62	71.3	574	16	US-10-413-432-18	Sequence 20, Appli
66	62	71.3	574	16	US-10-413-432-20	Sequence 22, Appli
67	62	71.3	574	16	US-10-413-432-22	Sequence 24, Appli
68	62	71.3	574	16	US-10-413-432-24	Sequence 26, Appli
69	62	71.3	574	16	US-10-413-432-26	Sequence 28, Appli
70	62	71.3	574	16	US-10-413-432-28	Sequence 30, Appli
71	62	71.3	574	16	US-10-413-432-30	Sequence 32, Appli
72	62	71.3	574	16	US-10-413-432-32	Sequence 34, Appli
73	62	71.3	574	16	US-10-413-432-34	Sequence 36, Appli
74	62	71.3	574	16	US-10-413-432-36	Sequence 38, Appli
75	62	71.3	574	16	US-10-413-432-38	Sequence 40, Appli
76	62	71.3	574	16	US-10-413-432-40	Sequence 42, Appli
77	62	71.3	574	16	US-10-413-432-42	Sequence 44, Appli
78	62	71.3	574	16	US-10-413-432-44	Sequence 46, Appli
79	62	71.3	574	16	US-10-413-432-46	Sequence 48, Appli
80	62	71.3	574	16	US-10-413-432-48	Sequence 50, Appli
81	62	71.3	574	16	US-10-413-432-50	Sequence 52, Appli
82	62	71.3	574	16	US-10-413-432-52	Sequence 54, Appli
83	62	71.3	574	16	US-10-413-432-54	Sequence 56, Appli
84	62	71.3	574	16	US-10-413-432-56	Sequence 58, Appli

85	62	71.3	574	16	US-10-324-466-2	Sequence 2, Appli	158	62	71.3	574	18	US-10-728-723-102	Sequence 102, App
86	62	71.3	574	16	US-10-324-466-4	Sequence 4, Appli	159	62	71.3	574	18	US-10-728-723-104	Sequence 104, App
87	62	71.3	574	16	US-10-324-466-6	Sequence 6, Appli	160	62	71.3	574	18	US-10-728-723-106	Sequence 106, App
88	62	71.3	574	16	US-10-324-466-8	Sequence 8, Appli	161	62	71.3	574	18	US-10-728-723-108	Sequence 108, App
89	62	71.3	574	16	US-10-324-466-10	Sequence 10, Appli	162	62	71.3	574	18	US-10-728-723-112	Sequence 112, App
90	62	71.3	574	16	US-10-324-466-12	Sequence 12, Appli	163	62	71.3	574	18	US-10-728-723-114	Sequence 114, App
91	62	71.3	574	16	US-10-324-466-14	Sequence 14, Appli	164	62	71.3	574	18	US-10-728-723-116	Sequence 116, App
92	62	71.3	574	16	US-10-324-466-16	Sequence 16, Appli	165	62	71.3	574	18	US-10-728-723-118	Sequence 118, App
93	62	71.3	574	16	US-10-324-466-18	Sequence 18, Appli	166	62	71.3	574	18	US-10-728-723-120	Sequence 120, App
94	62	71.3	574	16	US-10-324-466-20	Sequence 20, Appli	167	62	71.3	574	18	US-10-728-723-122	Sequence 122, App
95	62	71.3	574	16	US-10-324-466-22	Sequence 22, Appli	168	62	71.3	574	18	US-10-728-723-124	Sequence 124, App
96	62	71.3	574	16	US-10-324-466-24	Sequence 24, Appli	169	62	71.3	574	18	US-10-728-723-126	Sequence 126, App
97	62	71.3	574	16	US-10-324-466-26	Sequence 26, Appli	170	62	71.3	574	18	US-10-728-723-128	Sequence 128, App
98	62	71.3	574	16	US-10-324-466-28	Sequence 28, Appli	171	62	71.3	574	18	US-10-728-723-130	Sequence 130, App
99	62	71.3	574	16	US-10-324-466-30	Sequence 30, Appli	172	62	71.3	574	18	US-10-728-723-132	Sequence 132, App
100	62	71.3	574	16	US-10-324-466-32	Sequence 32, Appli	173	62	71.3	574	18	US-10-728-723-134	Sequence 134, App
101	62	71.3	574	16	US-10-324-466-34	Sequence 34, Appli	174	62	71.3	574	18	US-10-728-723-136	Sequence 136, App
102	62	71.3	574	16	US-10-324-466-36	Sequence 36, Appli	175	62	71.3	574	18	US-10-728-723-138	Sequence 138, App
103	62	71.3	574	16	US-10-324-466-38	Sequence 38, Appli	176	62	71.3	574	18	US-10-728-723-140	Sequence 140, App
104	62	71.3	574	16	US-10-324-466-40	Sequence 40, Appli	177	62	71.3	574	18	US-10-728-723-142	Sequence 142, App
105	62	71.3	574	16	US-10-324-466-42	Sequence 42, Appli	178	62	71.3	574	18	US-10-728-723-144	Sequence 144, App
106	62	71.3	574	16	US-10-324-466-44	Sequence 44, Appli	179	62	71.3	574	18	US-10-728-723-146	Sequence 146, App
107	62	71.3	574	16	US-10-324-466-46	Sequence 46, Appli	180	62	71.3	574	18	US-10-728-723-148	Sequence 148, App
108	62	71.3	574	16	US-10-324-466-48	Sequence 48, Appli	181	62	71.3	574	18	US-10-728-723-150	Sequence 150, App
109	62	71.3	574	16	US-10-324-466-50	Sequence 50, Appli	182	62	71.3	574	18	US-10-728-723-152	Sequence 152, App
110	62	71.3	574	16	US-10-324-466-52	Sequence 52, Appli	183	62	71.3	574	18	US-10-728-723-154	Sequence 154, App
111	62	71.3	574	16	US-10-326-892-2	Sequence 2, Appli	184	62	71.3	574	18	US-10-728-723-156	Sequence 156, App
112	62	71.3	574	18	US-10-728-723-2	Sequence 4, Appli	185	62	71.3	574	18	US-10-728-723-158	Sequence 158, App
113	62	71.3	574	18	US-10-728-723-4	Sequence 6, Appli	186	62	71.3	574	18	US-10-728-723-160	Sequence 160, App
114	62	71.3	574	18	US-10-728-723-6	Sequence 8, Appli	187	62	71.3	574	18	US-10-728-723-162	Sequence 162, App
115	62	71.3	574	18	US-10-728-723-8	Sequence 10, Appli	188	62	71.3	574	18	US-10-728-723-164	Sequence 164, App
116	62	71.3	574	18	US-10-728-723-10	Sequence 12, Appli	189	62	71.3	574	18	US-10-728-723-166	Sequence 166, App
117	62	71.3	574	18	US-10-728-723-12	Sequence 14, Appli	190	62	71.3	574	18	US-10-728-723-168	Sequence 168, App
118	62	71.3	574	18	US-10-728-723-14	Sequence 16, Appli	191	62	71.3	574	18	US-10-728-723-170	Sequence 170, App
119	62	71.3	574	18	US-10-728-723-16	Sequence 18, Appli	192	62	71.3	574	18	US-10-728-723-172	Sequence 172, App
120	62	71.3	574	18	US-10-728-723-18	Sequence 20, Appli	193	62	71.3	574	18	US-10-728-723-174	Sequence 174, App
121	62	71.3	574	18	US-10-728-723-20	Sequence 22, Appli	194	62	71.3	574	18	US-10-728-723-176	Sequence 176, App
122	62	71.3	574	18	US-10-728-723-22	Sequence 24, Appli	195	62	71.3	574	18	US-10-728-723-178	Sequence 178, App
123	62	71.3	574	18	US-10-728-723-24	Sequence 26, Appli	196	62	71.3	574	18	US-10-728-723-180	Sequence 180, App
124	62	71.3	574	18	US-10-728-723-26	Sequence 28, Appli	197	62	71.3	574	18	US-10-728-723-182	Sequence 182, App
125	62	71.3	574	18	US-10-728-723-28	Sequence 30, Appli	198	62	71.3	574	18	US-10-728-723-184	Sequence 184, App
126	62	71.3	574	18	US-10-728-723-30	Sequence 32, Appli	199	62	71.3	574	18	US-10-728-723-186	Sequence 186, App
127	62	71.3	574	18	US-10-728-723-32	Sequence 34, Appli	200	62	71.3	574	18	US-10-728-723-188	Sequence 188, App
128	62	71.3	574	18	US-10-728-723-34	Sequence 36, Appli	201	62	71.3	574	18	US-10-728-723-190	Sequence 190, App
129	62	71.3	574	18	US-10-728-723-36	Sequence 38, Appli	202	62	71.3	574	18	US-10-728-723-192	Sequence 192, App
130	62	71.3	574	18	US-10-728-723-38	Sequence 40, Appli	203	62	71.3	574	18	US-10-728-723-194	Sequence 194, App
131	62	71.3	574	18	US-10-728-723-40	Sequence 42, Appli	204	62	71.3	574	18	US-10-728-723-196	Sequence 196, App
132	62	71.3	574	18	US-10-728-723-42	Sequence 44, Appli	205	62	71.3	602	9	US-09-748-739A-2	Sequence 2, Appli
133	62	71.3	574	18	US-10-728-723-44	Sequence 46, Appli	206	62	71.3	602	17	US-10-991-321-34	Sequence 34, Appli
134	62	71.3	574	18	US-10-728-723-46	Sequence 48, Appli	207	58	66.7	42	9	US-09-155-076-11	Sequence 11, Appli
135	62	71.3	574	18	US-10-728-723-48	Sequence 50, Appli	208	57	65.5	43	9	US-09-155-076-13	Sequence 13, Appli
136	62	71.3	574	18	US-10-728-723-50	Sequence 52, Appli	209	57	65.5	47	9	US-09-155-076-12	Sequence 12, Appli
137	62	71.3	574	18	US-10-728-723-52	Sequence 54, Appli	210	56	64.4	574	9	US-09-748-739A-22	Sequence 22, Appli
138	62	71.3	574	18	US-10-728-723-54	Sequence 56, Appli	211	56	64.4	574	14	US-10-032-233-49	Sequence 49, Appli
139	62	71.3	574	18	US-10-728-723-56	Sequence 58, Appli	212	56	64.4	574	16	US-10-413-432-49	Sequence 49, Appli
140	62	71.3	574	18	US-10-728-723-58	Sequence 60, Appli	213	56	64.4	574	16	US-10-324-466-49	Sequence 49, Appli
141	62	71.3	574	18	US-10-728-723-60	Sequence 62, Appli	214	47	54.0	64	15	US-10-424-599-213127	Sequence 213127,
142	62	71.3	574	18	US-10-728-723-62	Sequence 64, Appli	215	46	52.9	268	17	US-10-424-599-213127	Sequence 213127,
143	62	71.3	574	18	US-10-728-723-64	Sequence 66, Appli	216	45	51.7	87	15	US-10-473-451-7	Sequence 7, Appli
144	62	71.3	574	18	US-10-728-723-66	Sequence 68, Appli	217	45	51.7	87	15	US-10-437-963-147788	Sequence 147788,
145	62	71.3	574	18	US-10-728-723-68	Sequence 70, Appli	218	45	51.7	440	15	US-10-243-552-560	Sequence 560, App
146	62	71.3	574	18	US-10-728-723-70	Sequence 72, Appli	219	44	50.6	141	16	US-10-425-115-255218	Sequence 255218,
147	62	71.3	574	18	US-10-728-723-72	Sequence 74, Appli	220	44	50.6	473	15	US-10-425-115-255218	Sequence 5476, Ap
148	62	71.3	574	18	US-10-728-723-74	Sequence 76, Appli	221	43	49.4	496	18	US-10-369-493-3476	Sequence 3476, A
149	62	71.3	574	18	US-10-728-723-76	Sequence 78, Appli	222	43	49.4	593	20	US-10-450-763-54092	Sequence 54092, A
150	62	71.3	574	18	US-10-728-723-78	Sequence 80, Appli	223	42	48.3	119	14	US-11-097-143-1662	Sequence 1662, Ap
151	62	71.3	574	18	US-10-728-723-80	Sequence 82, Appli	224	42	48.3	220	16	US-10-194-975-121	Sequence 121, App
152	62	71.3	574	18	US-10-728-723-82	Sequence 84, Appli	225	42	48.3	368	15	US-10-154-975-121	Sequence 211872,
153	62	71.3	574	18	US-10-728-723-84	Sequence 86, Appli	226	42	48.3	822	11	US-10-425-115-211872	Sequence 169816,
154	62	71.3	574	18	US-10-728-723-86	Sequence 88, Appli	227	42	48.3	822	11	US-09-826-312-12	Sequence 12, Appli
155	62	71.3	574	18	US-10-728-723-88	Sequence 90, Appli	228	42	48.3	822	14	US-09-833-245-932	Sequence 932, App
156	62	71.3	574	18	US-10-728-723-90	Sequence 92, Appli	229	42	48.3	822	14	US-10-108-767-12	Sequence 12, Appli
157	62	71.3	574	18	US-10-728-723-92	Sequence 94, Appli	230	42	48.3	822	17	US-10-152-156-12	Sequence 12, Appli
158	62	71.3	574	18	US-10-728-723-94	Sequence 96, Appli	231	42	48.3	822	17	US-10-835-096-12	Sequence 12, Appli
159	62	71.3	574	18	US-10-728-723-96	Sequence 98, Appli	232	42	48.3	1578	13	US-10-087-192-960	Sequence 960, App
160	62	71.3	574	18	US-10-728-723-98	Sequence 100, App	233	42	48.3				

231	42	48.3	1788	16	US-10-408-765A-2265	Sequence 2265, Ap	304	39	44.8	117	16	US-10-425-115-363781	Sequence 363781,
232	42	48.3	1788	16	US-10-719-993-840	Sequence 840, App	305	39	44.8	121	15	US-10-428-408A-8	Sequence 8, Appl
233	42	48.3	2152	13	US-10-087-192-957	Sequence 957, App	306	39	44.8	121	15	US-10-428-408A-23	Sequence 23, Appl
234	42	48.3	2214	16	US-10-719-993-839	Sequence 839, App	307	39	44.8	121	15	US-10-428-408A-24	Sequence 24, Appl
235	42	48.3	2214	16	US-10-719-993-841	Sequence 841, App	308	39	44.8	121	15	US-10-428-408A-25	Sequence 25, Appl
236	41	47.1	83	14	US-10-106-698-6992	Sequence 6992, Ap	309	39	44.8	121	15	US-10-428-408A-26	Sequence 26, Appl
237	41	47.1	93	16	US-10-425-115-285731	Sequence 285731, Ap	310	39	44.8	121	15	US-10-428-408A-27	Sequence 27, Appl
238	41	47.1	95	15	US-10-424-599-20743	Sequence 20743, Ap	311	39	44.8	121	15	US-10-428-894-8	Sequence 8, Appl
239	41	47.1	95	18	US-10-450-763-33834	Sequence 33834, A	312	39	44.8	121	15	US-10-428-894-23	Sequence 23, Appl
240	41	47.1	124	15	US-10-424-599-157901	Sequence 157901, A	313	39	44.8	121	15	US-10-428-894-24	Sequence 24, Appl
241	41	47.1	146	16	US-10-437-963-168165	Sequence 168165, A	314	39	44.8	121	15	US-10-428-894-25	Sequence 25, Appl
242	41	47.1	234	15	US-10-282-122A-52747	Sequence 52747, A	315	39	44.8	121	15	US-10-428-894-26	Sequence 26, Appl
243	41	47.1	327	15	US-10-266-829-97	Sequence 97, Appl	316	39	44.8	121	15	US-10-428-894-27	Sequence 27, Appl
244	41	47.1	327	18	US-10-878-523-97	Sequence 97, Appl	317	39	44.8	121	16	US-10-699-874-8	Sequence 8, Appl
245	41	47.1	349	15	US-10-266-829-96	Sequence 96, Appl	318	39	44.8	121	16	US-10-699-874-23	Sequence 23, Appl
246	41	47.1	349	18	US-10-878-523-96	Sequence 96, Appl	319	39	44.8	121	16	US-10-699-874-24	Sequence 24, Appl
247	41	47.1	389	16	US-10-808-807-6	Sequence 6, Appl	320	39	44.8	121	16	US-10-699-874-25	Sequence 25, Appl
248	41	47.1	414	11	US-09-833-245-2039	Sequence 2039, Ap	321	39	44.8	121	16	US-10-699-874-26	Sequence 26, Appl
249	41	47.1	414	14	US-10-157-031-369	Sequence 369, App	322	39	44.8	121	16	US-10-699-874-27	Sequence 27, Appl
250	41	47.1	414	15	US-10-266-829-53	Sequence 53, Appl	323	39	44.8	121	15	US-10-424-599-249961	Sequence 249961, A
251	41	47.1	414	18	US-10-878-523-53	Sequence 53, Appl	324	39	44.8	136	15	US-10-424-599-197566	Sequence 197566, A
252	41	47.1	509	17	US-10-732-923-23952	Sequence 23952, A	325	39	44.8	138	15	US-10-424-599-179783	Sequence 179783, A
253	41	47.1	511	16	US-10-686-947-166	Sequence 166, App	326	39	44.8	142	16	US-10-343-663A-58	Sequence 58, Appl
254	41	47.1	511	16	US-10-686-947-168	Sequence 168, App	327	39	44.8	142	16	US-09-738-626-4293	Sequence 4293, Ap
255	41	47.1	511	18	US-10-943-507-164	Sequence 164, App	328	39	44.8	151	9	US-10-425-114-66081	Sequence 66081, A
256	41	47.1	511	18	US-10-943-507-166	Sequence 166, App	329	39	44.8	176	16	US-10-437-963-163650	Sequence 163650, A
257	41	47.1	512	17	US-10-732-923-23950	Sequence 23950, A	330	39	44.8	181	16	US-10-437-963-114317	Sequence 114317, A
258	41	47.1	1252	17	US-10-732-923-8663	Sequence 8663, Ap	331	39	44.8	208	16	US-10-437-963-137235	Sequence 137235, A
259	41	47.1	1637	16	US-10-437-963-185778	Sequence 185778, A	332	39	44.8	208	16	US-10-767-701-59384	Sequence 59384, A
260	41	47.1	1654	16	US-10-437-963-115478	Sequence 115478, A	333	39	44.8	224	15	US-10-425-114-67726	Sequence 67726, A
261	40.5	46.6	510	15	US-10-369-493-21941	Sequence 21941, A	334	39	44.8	231	15	US-10-282-122A-71271	Sequence 71271, A
262	40	46.0	43	16	US-10-425-115-245011	Sequence 245011, A	335	39	44.8	232	16	US-10-425-115-321035	Sequence 321035, A
263	40	46.0	57	16	US-10-425-115-261534	Sequence 261534, A	336	39	44.8	235	15	US-10-437-963-141090	Sequence 141090, A
264	40	46.0	61	15	US-10-424-599-180467	Sequence 180467, A	337	39	44.8	238	15	US-10-282-122A-58008	Sequence 58008, A
265	40	46.0	76	16	US-10-425-115-213516	Sequence 213516, A	338	39	44.8	238	18	US-10-450-763-55134	Sequence 55134, A
266	40	46.0	84	15	US-10-424-599-258197	Sequence 258197, A	339	39	44.8	242	15	US-10-425-114-71285	Sequence 71285, A
267	40	46.0	124	14	US-10-016-986-66	Sequence 66, Appl	340	39	44.8	243	16	US-10-425-115-332444	Sequence 332444, A
268	40	46.0	124	14	US-10-016-986-67	Sequence 67, Appl	341	39	44.8	244	17	US-10-732-923-10558	Sequence 10558, A
269	40	46.0	124	14	US-10-016-986-68	Sequence 68, Appl	342	39	44.8	260	1036	Ap	Sequence 1036, Ap
270	40	46.0	124	14	US-10-016-986-130	Sequence 130, App	343	39	44.8	260	15	US-10-293-418-1036	Sequence 1036, Ap
271	40	46.0	124	16	US-10-494-676-1	Sequence 1, Appl	344	39	44.8	265	15	US-10-369-493-19948	Sequence 19948, A
272	40	46.0	146	14	US-10-016-986-155	Sequence 155, App	345	39	44.8	266	14	US-10-156-761-9087	Sequence 9087, Ap
273	40	46.0	146	15	US-10-410-907A-4	Sequence 4, Appl	346	39	44.8	272	15	US-10-282-122A-70320	Sequence 70320, A
274	40	46.0	153	16	US-10-425-115-206745	Sequence 206745, A	347	39	44.8	272	17	US-10-732-923-15603	Sequence 15603, A
275	40	46.0	186	17	US-10-644-277-98	Sequence 98, Appl	348	39	44.8	274	15	US-10-282-122A-71110	Sequence 71110, A
276	40	46.0	243	10	US-09-880-748-1406	Sequence 1406, Ap	349	39	44.8	274	15	US-10-424-599-164540	Sequence 164540, A
277	40	46.0	243	15	US-10-293-418-1406	Sequence 1406, Ap	350	39	44.8	277	17	US-10-732-923-18935	Sequence 18935, A
278	40	46.0	247	15	US-09-880-748-1384	Sequence 1384, Ap	351	39	44.8	284	18	US-10-724-972A-4311	Sequence 4311, Ap
279	40	46.0	247	15	US-10-293-418-1384	Sequence 1384, Ap	352	39	44.8	286	16	US-10-437-963-126697	Sequence 126697, A
280	40	46.0	256	15	US-10-418-182-2	Sequence 2, Appl	353	39	44.8	286	16	US-10-425-115-332447	Sequence 332447, A
281	40	46.0	303	14	US-10-059-261-7706	Sequence 7706, Ap	354	39	44.8	288	18	US-10-450-763-55912	Sequence 55912, A
282	40	46.0	331	16	US-10-627-649-169	Sequence 169, App	355	39	44.8	308	15	US-10-346-198-29	Sequence 29, Appl
283	40	46.0	331	16	US-10-627-649-169	Sequence 169, App	356	39	44.8	308	15	US-10-424-599-171033	Sequence 171033, A
284	40	46.0	442	16	US-10-437-963-190013	Sequence 190013, A	357	39	44.8	334	15	US-10-424-599-279458	Sequence 279458, A
285	40	46.0	471	15	US-10-282-122A-47473	Sequence 47473, A	358	39	44.8	345	16	US-10-424-599-279458	Sequence 279458, A
286	40	46.0	476	15	US-10-409-938-15	Sequence 15, Appl	359	39	44.8	364	16	US-10-767-701-46366	Sequence 46366, A
287	40	46.0	549	20	US-11-097-143-41442	Sequence 41442, A	360	39	44.8	373	16	US-10-437-963-130065	Sequence 130065, A
288	40	46.0	707	17	US-10-732-923-9959	Sequence 9959, Ap	361	39	44.8	374	16	US-10-437-963-102652	Sequence 102652, A
289	40	46.0	735	15	US-10-108-260A-4426	Sequence 4426, Ap	362	39	44.8	379	16	US-10-437-963-178769	Sequence 178769, A
290	40	46.0	820	16	US-10-437-963-177434	Sequence 177434, A	363	39	44.8	385	16	US-10-739-930-7553	Sequence 7553, Ap
291	39.5	45.4	142	16	US-10-437-963-108837	Sequence 108837, A	364	39	44.8	405	16	US-10-425-115-332445	Sequence 332445, A
292	39.5	45.4	339	10	US-09-922-225A-8	Sequence 8, Appl	365	39	44.8	406	17	US-10-732-923-105454	Sequence 10554, A
293	39.5	45.4	611	10	US-09-922-225A-8	Sequence 8, Appl	366	39	44.8	467	15	US-10-428-894-30	Sequence 30, Appl
294	39	44.8	34	15	US-10-424-599-240394	Sequence 240394, A	367	39	44.8	467	15	US-10-428-894-30	Sequence 30, Appl
295	39	44.8	48	15	US-10-424-599-187297	Sequence 187297, A	368	39	44.8	493	16	US-10-699-874-30	Sequence 30, Appl
296	39	44.8	68	10	US-09-764-891-2835	Sequence 2835, Ap	369	39	44.8	496	15	US-10-437-963-128550	Sequence 128550, A
297	39	44.8	71	15	US-10-424-599-281466	Sequence 281466, A	370	39	44.8	496	15	US-10-104-047-3006	Sequence 3006, Ap
298	39	44.8	97	15	US-10-424-599-277157	Sequence 277157, A	371	39	44.8	507	15	US-10-369-493-2083	Sequence 2083, Ap
299	39	44.8	109	15	US-10-276-774-1999	Sequence 1999, Ap	372	39	44.8	518	16	US-10-739-930-6281	Sequence 6281, Ap
300	39	44.8	112	18	US-10-450-763-47139	Sequence 47139, A	373	39	44.8	523	9	US-10-425-115-244480	Sequence 244480, A
301	39	44.8	114	15	US-10-424-599-155913	Sequence 155913, A	374	39	44.8	525	16	US-09-815-242-12419	Sequence 12419, A
302	39	44.8	114	16	US-10-425-115-332896	Sequence 332896, A	375	39	44.8	555	16	US-10-437-963-105383	Sequence 105383, A
303	39	44.8	115	16	US-10-767-701-63034	Sequence 63034, A	376	39	44.8	608	9	US-09-815-242-5688	Sequence 5688, Ap
							377	39	44.8	651	15	US-10-282-122A-43859	Sequence 43859, A

377	38.5	44.3	154	15	US-10-424-599-173286	Sequence 173286,	450	419	15	US-10-424-599-210085	Sequence 210085,
378	38.5	44.3	204	14	US-10-156-761-8754	Sequence 8754, Ap	451	532	18	US-10-477-720A-7	Sequence 7, Appli
379	38.5	44.3	270	14	US-10-138-701-42	Sequence 42, Appl	452	534	15	US-10-415-188-16	Sequence 16, Appl
380	38.5	44.3	270	16	US-10-823-785-42	Sequence 42, Appl	453	534	18	US-10-477-720A-2	Sequence 2, Appli
381	38.5	44.3	277	16	US-10-724-972A-7301	Sequence 7301, Ap	454	534	18	US-10-477-720A-5	Sequence 5, Appli
382	38.5	44.3	499	17	US-10-732-923-9838	Sequence 9838, Ap	455	539	20	US-11-097-143-1115	Sequence 1115, A
383	38	43.7	18	16	US-10-258-144-358	Sequence 358, App	456	582	15	US-10-424-599-152001	Sequence 152001,
384	38	43.7	26	16	US-10-258-144-359	Sequence 359, App	457	585	18	US-10-873-467-132	Sequence 132, App
385	38	43.7	35	15	US-10-424-599-233971	Sequence 233971,	458	588	16	US-10-425-115-220572	Sequence 220572,
386	38	43.7	42	9	US-09-864-761-42803	Sequence 42803, A	459	619	15	US-10-369-493-17065	Sequence 17065, A
387	38	43.7	51	15	US-10-424-599-223246	Sequence 223246,	460	659	16	US-10-437-963-128426	Sequence 128426,
388	38	43.7	56	15	US-10-424-599-252008	Sequence 252008,	461	740	15	US-10-357-567-23	Sequence 23, Appl
389	38	43.7	67	16	US-10-437-963-177243	Sequence 177243,	462	741	15	US-10-094-749-2276	Sequence 2276, Ap
390	38	43.7	67	16	US-10-425-115-358167	Sequence 358167,	463	751	16	US-10-437-963-200330	Sequence 200330,
391	38	43.7	76	14	US-10-106-698-8451	Sequence 8451, Ap	464	751	15	US-10-104-047-2507	Sequence 2507, Ap
392	38	43.7	76	14	US-10-425-115-348227	Sequence 348227,	465	863	15	US-10-374-780A-1622	Sequence 1622, Ap
393	38	43.7	85	15	US-10-424-599-200667	Sequence 200667,	466	863	15	US-10-412-699B-1655	Sequence 1655, Ap
394	38	43.7	88	16	US-10-437-963-188893	Sequence 188893,	467	864	15	US-10-357-567-28	Sequence 28, Appl
395	38	43.7	89	15	US-10-424-599-185505	Sequence 185505,	468	925	16	US-10-437-963-199232	Sequence 199232,
396	38	43.7	96	16	US-10-425-115-280421	Sequence 280421,	469	1090	16	US-10-437-963-103565	Sequence 103565,
397	38	43.7	108	16	US-10-425-115-118385	Sequence 118385,	470	1137	9	US-09-737-246-60	Sequence 60, Appl
398	38	43.7	114	17	US-10-732-923-14686	Sequence 14686, A	471	1202	9	US-09-737-246-8	Sequence 8, Appli
399	38	43.7	117	16	US-10-631-722-31	Sequence 31, Appl	472	1220	9	US-09-736-969A-14	Sequence 14, Appl
400	38	43.7	118	16	US-10-631-722-35	Sequence 35, Appl	473	1220	9	US-09-737-246-14	Sequence 14, Appl
401	38	43.7	118	16	US-10-631-722-40	Sequence 40, Appl	474	1220	9	US-09-736-960-14	Sequence 14, Appl
402	38	43.7	124	14	US-10-016-986-125	Sequence 125, App	475	1220	9	US-09-736-968A-14	Sequence 14, Appl
403	38	43.7	124	14	US-10-016-986-127	Sequence 127, App	476	1239	20	US-11-097-143-1701	Sequence 1701, Ap
404	38	43.7	124	14	US-10-016-986-131	Sequence 131, App	477	1310	15	US-10-334-143-22	Sequence 22, Appl
405	38	43.7	124	14	US-10-016-986-132	Sequence 132, App	478	1428	16	US-10-437-963-112113	Sequence 112113,
406	38	43.7	125	14	US-10-016-986-124	Sequence 124, App	479	1999	10	US-09-978-244A-8	Sequence 8, Appli
407	38	43.7	125	14	US-10-016-986-128	Sequence 128, App	480	2045	9	US-09-736-969A-95	Sequence 95, Appl
408	38	43.7	125	15	US-10-251-085B-155	Sequence 155, App	481	2045	9	US-09-737-246-103	Sequence 103, App
409	38	43.7	125	15	US-10-251-085B-156	Sequence 156, App	482	2045	9	US-09-736-960-92	Sequence 92, Appl
410	38	43.7	125	16	US-10-737-252-155	Sequence 155, App	483	2045	9	US-09-736-968A-109	Sequence 109, App
411	38	43.7	125	16	US-10-737-252-156	Sequence 156, App	484	2047	9	US-09-736-968A-2	Sequence 2, Appli
412	38	43.7	126	14	US-10-016-986-123	Sequence 123, App	485	2047	10	US-09-978-244A-31	Sequence 31, Appl
413	38	43.7	139	9	US-09-864-761-33721	Sequence 33721, A	486	2090	9	US-09-736-969A-93	Sequence 93, Appl
414	38	43.7	140	14	US-10-283-349-27	Sequence 27, Appl	487	2090	9	US-09-737-246-2	Sequence 2, Appli
415	38	43.7	140	14	US-10-283-349-63	Sequence 63, Appl	488	2090	9	US-09-737-246-101	Sequence 101, App
416	38	43.7	140	14	US-10-283-349-74	Sequence 74, Appl	489	2090	9	US-09-736-960-90	Sequence 90, Appl
417	38	43.7	140	14	US-10-283-349-78	Sequence 78, Appl	490	2090	9	US-09-736-968A-107	Sequence 107, App
418	38	43.7	140	14	US-10-283-349-83	Sequence 83, Appl	491	2090	10	US-09-978-244A-28	Sequence 28, Appl
419	38	43.7	149	16	US-10-437-963-115434	Sequence 115434,	492	2108	8	US-08-973-363-16	Sequence 16, Appl
420	38	43.7	150	16	US-10-425-115-312533	Sequence 312533,	493	2710	13	US-10-153-273-12	Sequence 12, Appl
421	38	43.7	155	16	US-10-767-701-52833	Sequence 52833, A	494	37.5	43.1	US-10-767-701-61792	Sequence 61792, A
422	38	43.7	156	14	US-10-044-569B-6	Sequence 6, Appli	495	37.5	43.1	US-10-767-701-52405	Sequence 52405, A
423	38	43.7	158	9	US-09-808-701A-20	Sequence 20, Appl	496	37.5	43.1	US-10-425-115-354529	Sequence 354529,
424	38	43.7	158	14	US-10-233-131-20	Sequence 20, Appl	497	37.5	43.1	US-10-424-599-218581	Sequence 218581,
425	38	43.7	158	15	US-10-240-145-72	Sequence 72, Appl	498	37.5	43.1	US-10-424-599-276918	Sequence 276918,
426	38	43.7	158	16	US-10-291-128-72	Sequence 72, Appl	499	37.5	43.1	US-10-425-115-206564	Sequence 206564,
427	38	43.7	185	16	US-10-437-963-148167	Sequence 148167,	500	37.5	43.1	US-10-424-599-209586	Sequence 209586,
428	38	43.7	187	14	US-10-171-040A-22	Sequence 22, Appl					
429	38	43.7	201	9	US-09-738-626-4372	Sequence 4372, Ap					
430	38	43.7	217	15	US-10-424-599-256925	Sequence 256925,					
431	38	43.7	240	20	US-11-097-143-24453	Sequence 24453, A					
432	38	43.7	241	9	US-09-730-374-2	Sequence 2, Appli					
433	38	43.7	241	15	US-10-704-206-2	Sequence 2, Appli					
434	38	43.7	272	15	US-10-264-237-1902	Sequence 1902, Ap					
435	38	43.7	319	14	US-10-259-165-56	Sequence 56, Appl					
436	38	43.7	319	14	US-10-259-165-402	Sequence 402, App					
437	38	43.7	319	15	US-10-424-599-278291	Sequence 278291,					
438	38	43.7	342	15	US-10-425-114-47952	Sequence 47952, A					
439	38	43.7	351	14	US-10-284-740-22	Sequence 22, Appl					
440	38	43.7	364	15	US-10-469-993-14	Sequence 14, Appl					
441	38	43.7	364	17	US-10-732-923-10543	Sequence 10543, A					
442	38	43.7	377	15	US-10-424-599-278313	Sequence 278313,					
443	38	43.7	382	16	US-10-425-115-187552	Sequence 187552,					
444	38	43.7	388	15	US-10-374-780A-1813	Sequence 1813, Ap					
445	38	43.7	388	16	US-10-437-963-161114	Sequence 161114,					
446	38	43.7	399	15	US-10-425-114-51954	Sequence 51954, A					
447	38	43.7	406	15	US-10-425-114-57801	Sequence 57801, A					
448	38	43.7	408	16	US-10-437-963-171710	Sequence 171710,					
449	38	43.7	413	15	US-10-104-047-2267	Sequence 2267, Ap					

RESULT 1

US-09-155-076-1

Sequence 1, Application US/09155076A

Sequence 16, Appl

Sequence 17, Appl

Sequence 18, Appl

Sequence 19, Appl

Sequence 20, Appl

Sequence 21, Appl

Sequence 22, Appl

Sequence 23, Appl

Sequence 24, Appl

Sequence 25, Appl

Sequence 26, Appl

Sequence 27, Appl

Sequence 28, Appl

Sequence 29, Appl

Sequence 30, Appl

Sequence 31, Appl

Sequence 32, Appl

Sequence 33, Appl

Sequence 34, Appl

Sequence 35, Appl

Sequence 36, Appl

Sequence 37, Appl

Sequence 38, Appl

Sequence 39, Appl

Sequence 40, Appl

Sequence 41, Appl

Sequence 42, Appl

Sequence 43, Appl

Sequence 44, Appl

Sequence 45, Appl

Sequence 46, Appl

Sequence 47, Appl

Sequence 48, Appl

Sequence 49, Appl

Sequence 50, Appl

Sequence 51, Appl

Sequence 52, Appl

Sequence 53, Appl

Sequence 54, Appl

Sequence 55, Appl

Sequence 56, Appl

Sequence 57, Appl

Sequence 58, Appl

Sequence 59, Appl

Sequence 60, Appl

Sequence 61, Appl

Sequence 62, Appl

Sequence 63, Appl

Sequence 64, Appl

Sequence 65, Appl

Sequence 66, Appl

Sequence 67, Appl

Sequence 68, Appl

Sequence 69, Appl

Sequence 70, Appl

Sequence 71, Appl

Sequence 72, Appl

Sequence 73, Appl

Sequence 74, Appl

Sequence 75, Appl

Sequence 76, Appl

Sequence 77, Appl

Sequence 78, Appl

Sequence 79, Appl

Sequence 80, Appl

Sequence 81, Appl

Sequence 82, Appl

Sequence 83, Appl

Sequence 84, Appl

Sequence 85, Appl

Sequence 86, Appl

Sequence 87, Appl

Sequence 88, Appl

Sequence 89, Appl

Sequence 90, Appl

Sequence 91, Appl

Sequence 92, Appl

Sequence 93, Appl

Sequence 94, Appl

Sequence 95, Appl

Sequence 96, Appl

Sequence 97, Appl

Sequence 98, Appl

Sequence 99, Appl

Sequence 100, Appl

Sequence 101, Appl

Sequence 102, Appl

Sequence 103, Appl

Sequence 104, Appl

Sequence 105, Appl

Sequence 106, Appl

Sequence 107, Appl

Sequence 108, Appl

Sequence 109, Appl

Sequence 110, Appl

Sequence 111, Appl

Sequence 112, Appl

Sequence 113, Appl

Sequence 114, Appl

Sequence 115, Appl

Sequence 116, Appl

Sequence 117, Appl

Sequence 118, Appl

Sequence 119, Appl

Sequence 120, Appl

Sequence 121, Appl

Sequence 122, Appl

Sequence 123, Appl

Sequence 124, Appl

Sequence 125, Appl

Sequence 126, Appl

Sequence 127, Appl

Sequence 128, Appl

Sequence 129, Appl

Sequence 130, Appl

Sequence 131, Appl

Sequence 132, Appl

Sequence 133, Appl

Sequence 134, Appl

Sequence 135, Appl

Sequence 136, Appl

Sequence 137, Appl

Sequence 138, Appl

Sequence 139, Appl

Sequence 140, Appl

Sequence 141, Appl

Sequence 142, Appl

Sequence 143, Appl

Sequence 144, Appl

Sequence 145, Appl

Sequence 146, Appl

Sequence 147, Appl

Sequence 148, Appl

Sequence 149, Appl

Sequence 150, Appl

Sequence 151, Appl

Sequence 152, Appl

Sequence 153, Appl

Sequence 154, Appl

Sequence 155, Appl

Sequence 156, Appl

Sequence 157, Appl

Sequence 158, Appl

Sequence 159, Appl

Sequence 160, Appl

Sequence 161, Appl

Sequence 162, Appl

Sequence 163, Appl

Sequence 164, Appl

Sequence 165, Appl

Sequence 166, Appl

Sequence 167, Appl

Sequence 168, Appl

Sequence 169, Appl

Sequence 170, Appl

Sequence 171, Appl

Sequence 172, Appl

Sequence 173, Appl

Sequence 174, Appl

Sequence 175, Appl

Sequence 176, Appl

Sequence 177, Appl

Sequence 178, Appl

Sequence 179, Appl

Sequence 180, Appl

Sequence 181, Appl

Sequence 182, Appl

Sequence 183, Appl

Sequence 184, Appl

Sequence 185, Appl

Sequence 186, Appl

Sequence 187, Appl

Sequence 188, Appl

Sequence 189, Appl

Sequence 190, Appl

Sequence 191, Appl

Sequence 192, Appl

Sequence 193, Appl

Sequence 194, Appl

Sequence 195, Appl

Sequence 196, Appl

Sequence 197, Appl

Sequence 198, Appl

Sequence 199, Appl

Sequence 200, Appl

Sequence 201, Appl

Sequence 202, Appl

Sequence 203, Appl

Sequence 204, Appl

Sequence 205, Appl

Sequence 206, Appl

Sequence 207, Appl

Sequence 208, Appl

Sequence 209, Appl

Sequence 210, Appl

Sequence 211, Appl

Sequence 212, Appl

Sequence 213, Appl

Sequence 214, Appl

Sequence 215, Appl

Sequence 216, Appl

Sequence 217, Appl

Sequence 218, Appl

Sequence 219, Appl

Sequence 220, Appl

Sequence 221, Appl

Sequence 222, Appl

Sequence 223, Appl

Sequence 224, Appl

Sequence 225, Appl

Sequence 226, Appl

Sequence 227, Appl

Sequence 228, Appl

Sequence 229, Appl

Sequence 230, Appl

Sequence 231, Appl

Sequence 232, Appl

Sequence 233, Appl

Sequence 234, Appl

Sequence 235, Appl

Sequence 236, Appl

Sequence 237, Appl

Sequence 238, Appl

Sequence 239, Appl

Sequence 240, Appl

Sequence 241, Appl

Sequence 242, Appl

Sequence 243, Appl

Sequence 244, Appl

Sequence 245, Appl

Sequence 246, Appl

Sequence 247, Appl

Sequence 248, Appl

Sequence 249, Appl

Sequence 250, Appl

Sequence 251, Appl

Sequence 252, Appl

Sequence 253, Appl

Sequence 254, Appl

Sequence 255, Appl

Sequence 256, Appl

Sequence 257, Appl

Sequence 258, Appl

Sequence 259, Appl

Sequence 260, Appl

Sequence 261, Appl

Sequence 262, Appl

Sequence 263, Appl

Sequence 264, Appl

Sequence 265, Appl

Sequence 266, Appl

Sequence 267, Appl

Sequence 268, Appl

Sequence 269, Appl

Sequence 270, Appl

Sequence 271, Appl

Sequence 272, Appl

Sequence 273, Appl

Sequence 274, Appl

Sequence 275, Appl

Sequence 276, Appl

Sequence 277, Appl

Sequence 278, Appl

Sequence 279, Appl

Sequence 280, Appl

Sequence 281, Appl

Sequence 282, Appl

Sequence 283, Appl

Sequence 284, Appl

Sequence 285, Appl

Sequence 286, Appl

Sequence 287, Appl

Sequence 288, Appl

Sequence 289, Appl

Sequence 290, Appl

Sequence 291, Appl

Sequence 292, Appl

Sequence 293, Appl

Sequence 294, Appl

Sequence 295, Appl

Sequence 296, Appl

Sequence 297, Appl

Sequence 298, Appl

Sequence 299, Appl

Sequence 30

ALIGNMENTS

RESULT 1

US-09-155-076-1

; Sequence 1, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PRPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155.076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-155-076-1

Query Match      100.0%; Score 87; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
   |||||
Db 1 AEFHRWSSYVHWK 14

RESULT 2
US-09-998-042-2
; Sequence 2, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
; APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
; TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: 7811/WO/99
; CURRENT APPLICATION NUMBER: US/09/998,042
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: HOMO SAPIENCE
US-09-998-042-2

Query Match      100.0%; Score 87; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
   |||||
Db 12 AEFHRWSSYVHWK 25

RESULT 3
US-09-155-076-6
; Sequence 6, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155.076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-6

Query Match      100.0%; Score 87; DB 9; Length 44;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
   |||||
Db 16 AEFHRWSSYVHWK 29

RESULT 4
US-09-155-076-8
; Sequence 8, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155.076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-8

Query Match      100.0%; Score 87; DB 9; Length 44;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
   |||||
Db 16 AEFHRWSSYVHWK 29

RESULT 5
US-09-155-076-9
; Sequence 9, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155.076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-9

Query Match      100.0%; Score 87; DB 9; Length 44;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
   |||||
Db 16 AEFHRWSSYVHWK 29

RESULT 6
US-09-155-076-10
; Sequence 10, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155.076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 53
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-10

Query Match      100.0%; Score 87; DB 9; Length 53;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEFHRWSSYVHWK 14
        |||||
Db       25 AEFHRWSSYVHWK 38

RESULT 7
US-09-155-076-7
; Sequence 7, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155,076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-7

Query Match      100.0%; Score 87; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEFHRWSSYVHWK 14
        |||||
Db       26 AEFHRWSSYVHWK 39

RESULT 8
US-09-998-042-8
; Sequence 8, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
; APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
; TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: 7811/WO/99
; CURRENT APPLICATION NUMBER: US/09/998,042
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ASP - peptide
US-09-998-042-8

Query Match      100.0%; Score 87; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEFHRWSSYVHWK 14
        |||||
Db       39 AEFHRWSSYVHWK 52
```

```
RESULT 9
US-10-116-275-258
; Sequence 258, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-116-275-258

Query Match      100.0%; Score 87; DB 15; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEFHRWSSYVHWK 14
        |||||
Db       586 AEFHRWSSYVHWK 599

RESULT 10
US-10-503-643-3
; Sequence 3, Application US/10503643
; Publication No. US20050176117A1
; GENERAL INFORMATION:
; APPLICANT: Robyn Joyce Russell
; APPLICANT: Rama Heidari
; APPLICANT: Alan Devonshire
; APPLICANT: Susan Jane Dorrian
; APPLICANT: John Graham Oakeshott
; TITLE OF INVENTION: Degradation of hydrophobic ester pesticides and toxins
; FILE REFERENCE: 69-04
; CURRENT APPLICATION NUMBER: US/10/503,643
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/AU02/00114
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Torpedo californica
; US-10-503-643-3

Query Match      92.0%; Score 80; DB 18; Length 576;
Best Local Similarity 92.3%; Pred. No. 0.0064;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 EFRHWSSYVHWK 14
        |||||
Db       549 EFRHWSSYVHWK 561

RESULT 11
US-10-503-691-4
; Sequence 4, Application US/10503691
; Publication No. US20050176118A1
; GENERAL INFORMATION:
; APPLICANT: John Graham Oakeshott
```

```
; APPLICANT: Alan Devonshire
; APPLICANT: Christopher Wayne Coppin
; APPLICANT: Rama Heidari
; APPLICANT: Susan Jane Dorrian
; APPLICANT: Robyn Joyce Russell
; TITLE OF INVENTION: Esterases with lipase activity
; FILE REFERENCE: 70-04
; CURRENT APPLICATION NUMBER: US/10/503,691
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/AU02/00113
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Torpedo californica
US-10-503-691-4

Query Match      92.0%; Score 80; DB 18; Length 576;
Best Local Similarity 92.3%; Pred. No. 0.0064;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EFHRWSSYVHWK 14
Db      549 EFHRWSSYVHWK 561

RESULT 12
US-09-998-042-3
; Sequence 3, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: 7811/WO/99
; CURRENT APPLICATION NUMBER: US/09/998,042
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-998-042-3

Query Match      89.7%; Score 78; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 FHRWSSYVHWK 14
Db      1 FHRWSSYVHWK 12

RESULT 13
US-09-748-739A-23
; Sequence 23, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus sp.
```

```
US-09-748-739A-23

Query Match      74.7%; Score 65; DB 9; Length 574;
Best Local Similarity 71.4%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWSNYMMDWK 558

RESULT 14
US-10-032-233-50
; Sequence 50, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-032-233-50

Query Match      74.7%; Score 65; DB 14; Length 574;
Best Local Similarity 71.4%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWSNYMMDWK 558

RESULT 15
US-10-413-432-50
; Sequence 50, Application US/10413432
; Publication No. US20040120939A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variant
; TITLE OF INVENTION: Polypeptides with Increased Catalytic Efficiency and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 5510
; CURRENT APPLICATION NUMBER: US/10/413,432
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 10/324,466
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-413-432-50

Query Match      74.7%; Score 65; DB 16; Length 574;
Best Local Similarity 71.4%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWSNYMMDWK 558

RESULT 16
```

```
US-10-324-466-50
; Sequence 50, Application US/10324466
; Publication No. US20040121970A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variant
; TITLE OF INVENTION: Polypeptides with Increased Catalytic Efficiency and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 5555
; CURRENT APPLICATION NUMBER: US/10/324,466
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/10/032,233
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-324-466-50

Query Match 74.7%; Score 65; DB 16; Length 574;
Best Local Similarity 71.4%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
Db 545 AGFHRWNNYMDWK 558
|||||:|:|

RESULT 17
US-09-155-076-15
; Sequence 15, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
; APPLICANT: Greenfield et al., Susan A.
; TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
; TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
; FILE REFERENCE: 98-0967*/WMC/00263
; CURRENT APPLICATION NUMBER: US/09/155,076A
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-15

Query Match 71.3%; Score 62; DB 9; Length 14;
Best Local Similarity 64.3%; Pred. No. 0.074;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
Db 1 AGFHRWNNYMDWK 14
|||||:|:|

RESULT 18
US-10-728-723-52
; Sequence 52, Application US/10728723
; Publication No. US20050136044A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants That
; TITLE OF INVENTION: Alter the Activity of Chemotherapeutic Agents
; FILE REFERENCE: 66797-395
; CURRENT APPLICATION NUMBER: US/10/728,723
; CURRENT FILING DATE: 2003-12-04
```

```
; PRIOR APPLICATION NUMBER: US 10/310,666
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic butyrylcholinesterase variant
; NAME/KEY: VARIANT
; LOCATION: (1)...(573)
; OTHER INFORMATION: Xaa = Ala
US-10-728-723-52

Query Match 71.3%; Score 62; DB 18; Length 573;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
Db 544 AGFHRWNNYMDWK 557
|||||:|:|

RESULT 19
US-10-728-723-92
; Sequence 92, Application US/10728723
; Publication No. US20050136044A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants That
; TITLE OF INVENTION: Alter the Activity of Chemotherapeutic Agents
; FILE REFERENCE: 66797-395
; CURRENT APPLICATION NUMBER: US/10/728,723
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 10/310,666
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic butyrylcholinesterase variant
; NAME/KEY: VARIANT
; LOCATION: (1)...(573)
; OTHER INFORMATION: Xaa = Ala
US-10-728-723-92

Query Match 71.3%; Score 62; DB 18; Length 573;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
Db 544 AGFHRWNNYMDWK 557
|||||:|:|

RESULT 20
US-10-728-723-110
; Sequence 110, Application US/10728723
; Publication No. US20050136044A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants That
; TITLE OF INVENTION: Alter the Activity of Chemotherapeutic Agents
; FILE REFERENCE: 66797-395
; CURRENT APPLICATION NUMBER: US/10/728,723
```



```
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 10/310,666
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic butyrylcholinesterase variant
; NAME/KEY: VARIANT
; LOCATION: (1)...(573)
; OTHER INFORMATION: Xaa = Ala
US-10-728-723-110

Query Match      71.3%; Score 62; DB 18; Length 573;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSVMVHWK 14
      | |||||::||: ||
Db      544 AGFHRWNNYMDWK 557

RESULT 21
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-4

Query Match      71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSVMVHWK 14
      | |||||::||: ||
Db      545 AGFHRWNNYMDWK 558

RESULT 22
US-09-748-739A-6
; Sequence 6, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-6

Query Match      71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSVMVHWK 14
      | |||||::||: ||
Db      545 AGFHRWNNYMDWK 558

RESULT 23
US-09-748-739A-8
; Sequence 8, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

Query Match      71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSVMVHWK 14
      | |||||::||: ||
Db      545 AGFHRWNNYMDWK 558

RESULT 24
US-09-748-739A-17
; Sequence 17, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-17

Query Match      71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSVMVHWK 14
      | |||||::||: ||
Db      545 AGFHRWNNYMDWK 558
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-20

Query Match 71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 545 AGFHRWNNYMDWK 558

RESULT 28
US-09-748-739A-21
; Sequence 21, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-748-739A-21

Query Match 71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 545 AGFHRWNNYMDWK 558

RESULT 29
US-09-997-209-89
; Sequence 89, Application US/09997209
; Publication No. US20030096401A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Eukaryotic Expression Libraries and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 5066
; CURRENT APPLICATION NUMBER: US/09/997,209
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,762
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-209-89

Query Match 71.3%; Score 62; DB 10; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 545 AGFHRWNNYMDWK 558

RESULT 26
US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-19

Query Match 71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 545 AGFHRWNNYMDWK 558

RESULT 27
US-09-748-739A-20
; Sequence 20, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-20

Query Match 71.3%; Score 62; DB 9; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 545 AGFHRWNNYMDWK 558

```

```

; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-6

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches      9; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 30
US-10-032-233-2
; Sequence 2, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-2

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches      9; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 31
US-10-032-233-4
; Sequence 4, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-4

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches      9; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 32
US-10-032-233-6
; Sequence 6, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-6

```

```

; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-6

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches      9; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 33
US-10-032-233-8
; Sequence 8, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-8

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches      9; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Qy      1 AEFHRWSSYVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 34
US-10-032-233-10
; Sequence 10, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-10

```

US-10-032-233-10

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | : | : |
Db 545 AGFHRWNMMMDWK 558

RESULT 35

US-10-032-233-12
; Sequence 12, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-12

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | : | : |
Db 545 AGFHRWNMMMDWK 558

RESULT 36

US-10-032-233-14
; Sequence 14, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-14

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | : | : |
Db 545 AGFHRWNMMMDWK 558

RESULT 37

US-10-032-233-16
; Sequence 16, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-16

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | : | : |
Db 545 AGFHRWNMMMDWK 558

RESULT 38

US-10-032-233-18
; Sequence 18, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-18

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | : | : |
Db 545 AGFHRWNMMMDWK 558

RESULT 39

US-10-032-233-20
; Sequence 20, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233

```
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-20

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYMWVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 40
US-10-032-233-22
; Sequence 22, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-22

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYMWVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 41
US-10-032-233-24
; Sequence 24, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-24

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYMWVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 42
US-10-032-233-26
; Sequence 26, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-26

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYMWVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 43
US-10-032-233-28
; Sequence 28, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-28

Query Match      71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AEFHRWSSYMWVHWK 14
Db      545 AGFHRWNNYMDWK 558

RESULT 44
US-10-032-233-30
```

Fri Oct 14 11:36:45 2005

; Sequence 30, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-30

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | | | | |
Db 545 AGFHRWNNYMDWK 558

RESULT 45
US-10-032-233-32
; Sequence 32, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Pancook, James D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants with
; TITLE OF INVENTION: Increased Catalytic Efficiency and Methods of Use
; FILE REFERENCE: P-IX 4642
; CURRENT APPLICATION NUMBER: US/10/032,233
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-32

Query Match 71.3%; Score 62; DB 14; Length 574;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | | | | |
Db 545 AGFHRWNNYMDWK 558

Search completed: October 12, 2005, 10:34:48
Job time : 169 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:15:43 ; Search time 41 Seconds
(without alignments)
25.490 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRWSSYVHWK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	40	2	US-08-370-156-25
2	87	100.0	45	2	US-08-370-156-7
3	87	100.0	45	2	US-08-370-156-8
4	87	100.0	45	3	US-08-990-065-21
5	87	100.0	45	3	US-08-975-084-5
6	87	100.0	45	4	US-09-380-532-11
7	87	100.0	614	1	US-07-732-962A-2
8	87	100.0	614	2	US-08-370-156-2
9	87	100.0	614	3	US-08-446-100-19
10	87	100.0	614	3	US-08-446-100-20
11	87	100.0	614	3	US-08-446-100-21
12	87	100.0	614	3	US-08-446-100-22
13	87	100.0	614	3	US-08-446-100-23
14	87	100.0	614	3	US-08-446-100-25
15	87	100.0	614	3	US-08-814-095-2
16	87	100.0	614	5	PCT-US92-06106-2
17	87	100.0	645	4	US-09-949-016-7063
18	87	100.0	645	4	US-09-949-016-7064
19	80	92.0	575	1	US-08-348-920-1
20	80	92.0	575	1	US-08-348-920-2
21	62	71.3	572	6	5200183-5
22	62	71.3	572	6	5200183-5
23	62	71.3	573	6	5215909-12
24	62	71.3	573	6	5215909-12
25	62	71.3	602	3	US-08-446-100-1
26	62	71.3	602	3	US-08-446-100-2
27	62	71.3	602	3	US-08-446-100-3

28	62	71.3	602	3	US-08-446-100-4	Sequence 4, Appli
29	62	71.3	602	3	US-08-446-100-5	Sequence 5, Appli
30	62	71.3	602	3	US-08-446-100-6	Sequence 6, Appli
31	62	71.3	602	3	US-08-446-100-7	Sequence 7, Appli
32	62	71.3	602	3	US-08-446-100-8	Sequence 8, Appli
33	62	71.3	602	3	US-08-446-100-9	Sequence 9, Appli
34	62	71.3	602	3	US-08-446-100-10	Sequence 10, Appli
35	62	71.3	602	3	US-08-446-100-11	Sequence 11, Appli
36	62	71.3	602	3	US-08-446-100-12	Sequence 12, Appli
37	62	71.3	602	3	US-08-446-100-13	Sequence 13, Appli
38	62	71.3	602	3	US-08-446-100-14	Sequence 14, Appli
39	62	71.3	602	3	US-08-446-100-15	Sequence 15, Appli
40	62	71.3	602	3	US-08-446-100-16	Sequence 16, Appli
41	62	71.3	602	3	US-08-446-100-17	Sequence 17, Appli
42	62	71.3	602	3	US-08-446-100-18	Sequence 18, Appli
43	62	71.3	602	3	US-08-446-100-24	Sequence 24, Appli
44	62	71.3	602	3	US-09-334-489-3	Sequence 3, Appli
45	62	71.3	602	3	US-09-334-489-4	Sequence 4, Appli
46	62	71.3	602	6	5215909-11	Patent No. 5215909
47	62	71.3	602	6	5215909-11	Patent No. 5215909
48	62	71.3	635	6	5215909-10	Patent No. 5215909
49	62	71.3	635	6	5215909-10	Patent No. 5215909
50	62	71.3	643	4	US-09-949-016-11146	Sequence 11146, A
51	43	49.4	86	4	US-09-248-796A-24358	Sequence 24358, A
52	42.5	48.9	272	4	US-09-248-796A-16385	Sequence 16385, A
53	42	48.3	657	3	US-09-306-593-2	Sequence 2, Appli
54	42	48.3	822	4	US-09-826-312A-12	Sequence 12, Appli
55	42	48.3	822	4	US-09-542-497A-12	Sequence 12, Appli
56	42	48.3	1788	2	US-08-962-284-2	Sequence 2, Appli
57	42	48.3	1792	2	US-08-962-284-4	Sequence 4, Appli
58	41.5	47.7	416	4	US-09-270-767-45333	Sequence 45333, A
59	40.5	46.6	166	4	US-09-134-000C-4007	Sequence 4007, Ap
60	40.5	46.6	510	1	US-08-742-273-2	Sequence 2, Appli
61	40.5	46.6	510	1	US-09-763-331-2	Sequence 2, Appli
62	40	46.0	71	4	US-09-270-767-40357	Sequence 40357, A
63	40	46.0	71	4	US-09-270-767-55573	Sequence 55573, A
64	40	46.0	124	1	US-08-276-852-66	Sequence 66, Appli
65	40	46.0	124	1	US-08-276-852-67	Sequence 67, Appli
66	40	46.0	124	1	US-08-276-852-68	Sequence 68, Appli
67	40	46.0	124	1	US-08-276-852-130	Sequence 130, App
68	40	46.0	124	1	US-08-899-575-66	Sequence 66, Appli
69	40	46.0	124	1	US-08-899-575-67	Sequence 67, Appli
70	40	46.0	124	1	US-08-899-575-68	Sequence 68, Appli
71	40	46.0	124	1	US-08-899-575-130	Sequence 130, App
72	40	46.0	124	1	US-08-899-575-66	Sequence 66, Appli
73	40	46.0	124	1	US-08-899-575-67	Sequence 67, Appli
74	40	46.0	124	1	US-08-899-575-68	Sequence 68, Appli
75	40	46.0	124	1	US-08-899-575-130	Sequence 130, App
76	40	46.0	124	3	US-08-591-632-1	Sequence 1, Appli
77	40	46.0	124	3	US-09-611-451-1	Sequence 1, Appli
78	40	46.0	124	5	PCT-US95-08743-66	Sequence 66, Appli
79	40	46.0	124	5	PCT-US95-08743-67	Sequence 67, Appli
80	40	46.0	124	5	PCT-US95-08743-68	Sequence 68, Appli
81	40	46.0	124	5	PCT-US95-08743-130	Sequence 130, App
82	40	46.0	146	1	US-08-276-852-155	Sequence 155, App
83	40	46.0	146	1	US-08-899-575-155	Sequence 155, App
84	40	46.0	146	1	US-08-899-575-155	Sequence 155, App
85	40	46.0	146	5	PCT-US95-08743-155	Sequence 155, App
86	40	46.0	166	4	US-09-270-767-33910	Sequence 33910, A
87	40	46.0	245	4	US-09-538-092-337	Sequence 337, App
88	40	46.0	413	4	US-09-543-681A-6035	Sequence 6035, Ap
89	39.5	45.4	31	4	US-09-270-767-45808	Sequence 45808, A
90	39.5	45.4	31	4	US-09-270-767-61334	Sequence 61334, A
91	39	44.8	124	3	US-08-591-632-3	Sequence 3, Appli
92	39	44.8	124	3	US-08-591-632-5	Sequence 5, Appli
93	39	44.8	124	3	US-08-591-632-54	Sequence 54, Appli
94	39	44.8	124	3	US-08-591-632-55	Sequence 55, Appli
95	39	44.8	124	3	US-08-591-632-56	Sequence 56, Appli
96	39	44.8	124	3	US-08-591-632-57	Sequence 57, Appli
97	39	44.8	124	3	US-08-591-632-58	Sequence 58, Appli
98	39	44.8	124	3	US-08-591-632-59	Sequence 59, Appli
99	39	44.8	124	3	US-08-591-632-60	Sequence 60, Appli
100	39	44.8	124	3	US-08-591-632-61	Sequence 61, Appli

101	39	44.8	124	3	US-09-611-451-3	Sequence 3, Appl	174	38	43.7	2710	2	US-08-487-826B-12	Sequence 12, Appl
102	39	44.8	124	3	US-09-611-451-5	Sequence 5, Appl	175	38	43.7	2710	3	US-09-210-288-12	Sequence 12, Appl
103	39	44.8	124	3	US-09-611-451-54	Sequence 54, Appl	176	38	43.7	3060	3	US-08-487-826B-14	Sequence 14, Appl
104	39	44.8	124	3	US-09-611-451-55	Sequence 55, Appl	177	37.5	43.1	3077	6	5223423-2	Patent No. 5223423
105	39	44.8	124	3	US-09-611-451-56	Sequence 56, Appl	178	37.5	43.1	3077	6	5223423-2	Patent No. 5223423
106	39	44.8	124	3	US-09-611-451-57	Sequence 57, Appl	179	37	42.5	26	2	US-08-620-151-39	Sequence 39, Appl
107	39	44.8	124	3	US-09-611-451-58	Sequence 58, Appl	180	37	42.5	69	4	US-09-149-476-617	Sequence 617, Appl
108	39	44.8	124	3	US-09-611-451-59	Sequence 59, Appl	181	37	42.5	89	3	US-09-217-228-33	Sequence 33, Appl
109	39	44.8	124	3	US-09-611-451-60	Sequence 60, Appl	182	37	42.5	110	3	US-08-545-809A-129	Sequence 129, Appl
110	39	44.8	124	3	US-09-611-451-61	Sequence 61, Appl	183	37	42.5	114	4	US-09-726-219A-219	Sequence 219, Appl
111	39	44.8	124	3	US-08-392-419-2	Sequence 2, Appl	184	37	42.5	117	5	PCT-US93-11611-6	Sequence 6, Appl
112	39	44.8	124	3	US-09-252-991A-32897	Sequence 32897, A	185	37	42.5	117	5	PCT-US93-11611-7	Sequence 7, Appl
113	39	44.8	238	4	US-09-107-532A-5419	Sequence 5419, Ap	186	37	42.5	119	2	US-08-737-560A-10	Sequence 10, Appl
114	39	44.8	239	3	US-09-134-001C-4165	Sequence 4165, Ap	187	37	42.5	119	4	US-09-438-954-2	Sequence 2, Appl
115	39	44.8	276	4	US-09-710-279-1482	Sequence 1482, Ap	188	37	42.5	119	4	US-09-438-954-4	Sequence 4, Appl
116	39	44.8	433	4	US-09-252-991A-20728	Sequence 20728, A	189	37	42.5	119	4	US-09-438-954-39	Sequence 39, Appl
117	38.5	44.3	154	4	US-09-489-039A-13313	Sequence 13313, A	190	37	42.5	124	3	US-08-591-632-45	Sequence 45, Appl
118	38.5	44.3	191	4	US-09-710-279-638	Sequence 638, App	191	37	42.5	124	3	US-08-591-632-89	Sequence 89, Appl
119	38.5	44.3	270	4	US-10-138-701-42	Sequence 42, Appl	192	37	42.5	124	3	US-08-591-632-91	Sequence 91, Appl
120	38.5	44.3	277	3	US-09-134-001C-5558	Sequence 5558, Ap	193	37	42.5	124	3	US-09-611-451-45	Sequence 45, Appl
121	38	43.7	66	4	US-09-107-532A-5433	Sequence 5433, Ap	194	37	42.5	124	3	US-09-611-451-89	Sequence 89, Appl
122	38	43.7	122	2	US-07-916-098A-10	Sequence 10, Appl	195	37	42.5	124	3	US-09-611-451-91	Sequence 91, Appl
123	38	43.7	124	1	US-08-276-852-125	Sequence 125, App	196	37	42.5	128	4	US-09-615-192A-288	Sequence 288, App
124	38	43.7	124	1	US-08-276-852-127	Sequence 127, App	197	37	42.5	136	5	PCT-US93-11611-4	Sequence 4, Appl
125	38	43.7	124	1	US-08-276-852-131	Sequence 131, App	198	37	42.5	136	5	PCT-US93-11611-11	Sequence 11, Appl
126	38	43.7	124	1	US-08-276-852-132	Sequence 132, App	199	37	42.5	142	4	US-09-564-329A-13	Sequence 13, Appl
127	38	43.7	124	1	US-08-899-575-125	Sequence 125, App	200	37	42.5	142	4	US-09-963-620-13	Sequence 13, Appl
128	38	43.7	124	1	US-08-899-575-127	Sequence 127, App	201	37	42.5	142	4	US-09-855-632-13	Sequence 13, Appl
129	38	43.7	124	1	US-08-899-575-131	Sequence 131, App	202	37	42.5	142	4	US-09-934-773-13	Sequence 13, Appl
130	38	43.7	124	1	US-08-899-575-132	Sequence 132, App	203	37	42.5	162	4	US-09-244-111-6	Sequence 6, Appl
131	38	43.7	124	1	US-08-899-575-135	Sequence 135, App	204	37	42.5	279	4	US-09-252-991A-24419	Sequence 24419, A
132	38	43.7	124	1	US-08-899-575-135	Sequence 125, App	205	37	42.5	321	4	US-09-688-019-2	Sequence 2, Appl
133	38	43.7	124	1	US-08-899-575-137	Sequence 137, App	206	37	42.5	327	1	US-08-375-962B-12	Sequence 12, Appl
134	38	43.7	124	1	US-08-899-575-131	Sequence 131, App	207	37	42.5	327	1	US-08-562-114B-12	Sequence 12, Appl
135	38	43.7	124	5	PCT-US95-08743-125	Sequence 125, App	208	37	42.5	327	3	US-08-739-594A-12	Sequence 12, Appl
136	38	43.7	124	5	PCT-US95-08743-127	Sequence 127, App	209	37	42.5	327	3	US-09-538-092-924	Sequence 924, Appl
137	38	43.7	124	5	PCT-US95-08743-131	Sequence 131, App	210	37	42.5	327	4	US-09-538-092-924	Sequence 924, Appl
138	38	43.7	124	5	PCT-US95-08743-132	Sequence 132, App	211	37	42.5	355	3	US-08-875-811-41	Sequence 41, Appl
139	38	43.7	125	1	US-08-276-852-124	Sequence 124, App	212	37	42.5	355	3	US-08-875-811-49	Sequence 49, Appl
140	38	43.7	125	1	US-08-276-852-128	Sequence 128, App	213	37	42.5	355	3	US-08-875-811-64	Sequence 64, Appl
141	38	43.7	125	1	US-08-899-575-124	Sequence 124, App	214	37	42.5	358	3	US-08-875-811-45	Sequence 45, Appl
142	38	43.7	125	1	US-08-899-575-128	Sequence 128, App	215	37	42.5	358	3	US-08-875-811-51	Sequence 51, Appl
143	38	43.7	125	1	US-08-899-575-124	Sequence 124, App	216	37	42.5	360	3	US-08-875-811-47	Sequence 47, Appl
144	38	43.7	125	1	US-08-899-575-128	Sequence 128, App	217	37	42.5	369	3	US-08-875-811-43	Sequence 43, Appl
145	38	43.7	125	5	PCT-US95-08743-124	Sequence 124, App	218	37	42.5	379	4	US-09-107-532A-6080	Sequence 6080, Ap
146	38	43.7	125	5	PCT-US95-08743-128	Sequence 128, App	219	37	42.5	428	4	US-09-270-767-45855	Sequence 45855, A
147	38	43.7	126	1	US-08-276-852-123	Sequence 123, App	220	37	42.5	428	4	US-09-134-000C-5376	Sequence 5376, Ap
148	38	43.7	126	1	US-08-899-575-123	Sequence 123, App	221	37	42.5	508	4	US-09-949-016-9414	Sequence 9414, Ap
149	38	43.7	126	1	US-08-899-575-123	Sequence 123, App	222	37	42.5	661	4	US-09-538-092-969	Sequence 969, App
150	38	43.7	126	5	PCT-US95-08743-123	Sequence 123, App	223	37	42.5	661	4	US-09-538-092-969	Sequence 969, App
151	38	43.7	140	3	US-08-836-561-27	Sequence 27, Appl	224	37	42.5	703	4	US-09-248-796A-17102	Sequence 17102, A
152	38	43.7	140	3	US-08-836-561-63	Sequence 63, Appl	225	36.5	42.0	356	3	US-09-235-103-2	Sequence 2, Appl
153	38	43.7	140	3	US-08-836-561-74	Sequence 74, Appl	226	36	41.4	9	3	US-09-139-802-21	Sequence 21, Appl
154	38	43.7	140	3	US-08-836-561-78	Sequence 78, Appl	227	36	41.4	9	4	US-09-659-786-21	Sequence 21, Appl
155	38	43.7	140	3	US-08-836-561-83	Sequence 83, Appl	228	36	41.4	9	4	US-08-926-914-21	Sequence 21, Appl
156	38	43.7	140	4	US-09-434-122-27	Sequence 27, Appl	229	36	41.4	10	2	US-08-556-597-145	Sequence 145, App
157	38	43.7	140	4	US-09-434-122-63	Sequence 63, Appl	230	36	41.4	91	4	US-10-088-548-4	Sequence 4, Appl
158	38	43.7	140	4	US-09-434-122-74	Sequence 74, Appl	231	36	41.4	108	2	US-08-273-146-57	Sequence 57, Appl
159	38	43.7	140	4	US-09-434-122-78	Sequence 78, Appl	232	36	41.4	110	4	US-09-270-767-45951	Sequence 45951, A
160	38	43.7	140	4	US-09-434-122-83	Sequence 83, Appl	233	36	41.4	111	3	US-08-881-037-15	Sequence 15, Appl
161	38	43.7	158	4	US-09-808-701A-20	Sequence 20, Appl	234	36	41.4	114	4	US-09-726-219A-230	Sequence 230, App
162	38	43.7	235	4	US-09-902-540-11835	Sequence 11835, A	235	36	41.4	114	4	US-09-726-219A-231	Sequence 231, App
163	38	43.7	285	4	US-09-252-991A-22267	Sequence 22267, A	236	36	41.4	115	4	US-09-726-219A-216	Sequence 216, App
164	38	43.7	364	4	US-09-653-375B-2	Sequence 2, Appl	237	36	41.4	116	2	US-08-561-521-41	Sequence 41, Appl
165	38	43.7	434	4	US-09-543-681A-7154	Sequence 7154, Ap	238	36	41.4	116	5	PCT-US95-01219-41	Sequence 41, Appl
166	38	43.7	467	2	US-07-916-098A-45	Sequence 45, App	239	36	41.4	119	3	US-08-881-037-60	Sequence 60, Appl
167	38	43.7	617	4	US-09-252-991A-23418	Sequence 23418, A	240	36	41.4	121	3	US-08-579-378A-7	Sequence 7, Appl
168	38	43.7	740	3	US-09-323-872A-23	Sequence 23, Appl	241	36	41.4	121	3	US-08-579-378A-8	Sequence 8, Appl
169	38	43.7	740	4	US-09-072-433-15	Sequence 15, Appl	242	36	41.4	121	5	PCT-US93-11612-7	Sequence 7, Appl
170	38	43.7	803	4	US-09-270-767-41698	Sequence 41698, A	243	36	41.4	125	2	US-08-665-202-44	Sequence 44, Appl
171	38	43.7	864	3	US-09-323-872A-28	Sequence 28, Appl	244	36	41.4	125	2	US-08-665-202-45	Sequence 45, Appl
172	38	43.7	864	4	US-09-072-433-16	Sequence 16, Appl	245	36	41.4	125	2	US-08-665-202-46	Sequence 46, Appl
173	38	43.7	2710	2	US-08-568-459A-12	Sequence 12, Appl	246	36	41.4	125	2	US-08-665-202-46	Sequence 46, Appl

247	36	41.4	125	2	US-08-665-202-47	Sequence 47, Appl	320	36	41.4	944	4	US-09-107-532A-4854	Sequence 4864, Ap
248	36	41.4	125	2	US-08-665-202-48	Sequence 48, Appl	321	35.5	40.8	78	4	US-09-270-767-49829	Sequence 4864, Ap
249	36	41.4	125	2	US-08-665-202-49	Sequence 49, Appl	322	35.5	40.8	78	4	US-09-270-767-49846	Sequence 4864, A
250	36	41.4	125	2	US-08-665-202-50	Sequence 50, Appl	323	35.5	40.8	124	4	US-09-270-767-61775	Sequence 61775, A
251	36	41.4	125	2	US-08-665-202-51	Sequence 51, Appl	324	35.5	40.8	216	4	US-09-489-039A-8059	Sequence 8059, Ap
252	36	41.4	125	2	US-08-665-202-52	Sequence 52, Appl	325	35.5	40.8	218	4	US-08-336-031-4	Sequence 4, Appl
253	36	41.4	125	2	US-08-665-202-53	Sequence 53, Appl	326	35.5	40.8	218	5	PCT-US95-06725-4	Sequence 4, Appl
254	36	41.4	125	2	US-08-665-202-54	Sequence 54, Appl	327	35.5	40.8	403	4	US-09-489-039A-12723	Sequence 12723, A
255	36	41.4	125	2	US-08-665-202-55	Sequence 55, Appl	328	35.5	40.8	411	2	US-08-336-031-2	Sequence 2, Appl
256	36	41.4	125	2	US-08-665-202-56	Sequence 56, Appl	329	35.5	40.8	411	2	US-08-902-853-7	Sequence 7, Appl
257	36	41.4	125	2	US-08-665-202-57	Sequence 57, Appl	330	35.5	40.8	411	5	PCT-US95-06725-2	Sequence 2, Appl
258	36	41.4	125	2	US-08-665-202-58	Sequence 58, Appl	331	35.5	40.8	491	4	US-09-107-532A-6115	Sequence 6115, Ap
259	36	41.4	125	2	US-08-665-202-59	Sequence 59, Appl	332	35	40.2	26	2	US-08-620-151-33	Sequence 33, Appl
260	36	41.4	125	4	US-09-315-574-44	Sequence 44, Appl	333	35	40.2	38	6	5262332-1	Patent No. 5262332
261	36	41.4	125	4	US-09-315-574-45	Sequence 45, Appl	334	35	40.2	38	6	5262332-1	Patent No. 5262332
262	36	41.4	125	4	US-09-315-574-46	Sequence 46, Appl	335	35	40.2	51	4	US-09-902-540-13339	Sequence 13339, A
263	36	41.4	125	4	US-09-315-574-47	Sequence 47, Appl	336	35	40.2	62	3	US-09-134-001C-4436	Sequence 4436, A
264	36	41.4	125	4	US-09-315-574-48	Sequence 48, Appl	337	35	40.2	84	3	US-08-928-383B-16	Sequence 16, Appl
265	36	41.4	125	4	US-09-315-574-49	Sequence 49, Appl	338	35	40.2	98	1	US-08-211-202-118	Sequence 118, App
266	36	41.4	125	4	US-09-315-574-50	Sequence 50, Appl	339	35	40.2	100	2	US-08-308-494A-15	Sequence 15, Appl
267	36	41.4	125	4	US-09-315-574-51	Sequence 51, Appl	340	35	40.2	102	4	US-09-640-211A-882	Sequence 882, App
268	36	41.4	125	4	US-09-315-574-52	Sequence 52, Appl	341	35	40.2	110	4	US-09-343-698-8	Sequence 8, Appl
269	36	41.4	125	4	US-09-315-574-53	Sequence 53, Appl	342	35	40.2	110	4	US-08-325-955-8	Sequence 8, Appl
270	36	41.4	125	4	US-09-315-574-54	Sequence 54, Appl	343	35	40.2	116	1	US-07-634-278-6	Sequence 6, Appl
271	36	41.4	125	4	US-09-315-574-55	Sequence 55, Appl	344	35	40.2	116	1	US-08-211-202-141	Sequence 141, App
272	36	41.4	125	4	US-09-315-574-56	Sequence 56, Appl	345	35	40.2	116	1	US-08-477-728-6	Sequence 6, Appl
273	36	41.4	125	4	US-09-315-574-57	Sequence 57, Appl	346	35	40.2	116	1	US-08-474-040-6	Sequence 6, Appl
274	36	41.4	125	4	US-09-315-574-58	Sequence 58, Appl	347	35	40.2	116	1	US-08-487-200-6	Sequence 6, Appl
275	36	41.4	125	4	US-09-315-574-59	Sequence 59, Appl	348	35	40.2	116	3	US-08-484-537-6	Sequence 6, Appl
276	36	41.4	129	2	US-08-665-202-32	Sequence 32, Appl	349	35	40.2	117	3	US-09-025-769B-24	Sequence 24, Appl
277	36	41.4	129	4	US-08-665-202-32	Sequence 32, Appl	350	35	40.2	117	4	US-09-430-070A-24	Sequence 24, Appl
278	36	41.4	135	1	US-08-137-117D-27	Sequence 27, Appl	351	35	40.2	117	4	US-09-490-153-24	Sequence 24, Appl
279	36	41.4	135	1	US-08-137-117D-100	Sequence 100, App	352	35	40.2	117	4	US-09-490-324-24	Sequence 24, Appl
280	36	41.4	135	1	US-08-137-117D-102	Sequence 102, App	353	35	40.2	118	3	US-08-545-809A-145	Sequence 145, App
281	36	41.4	135	1	US-08-137-117D-112	Sequence 112, App	354	35	40.2	119	1	US-08-331-398A-46	Sequence 46, Appl
282	36	41.4	135	2	US-08-436-717-27	Sequence 27, Appl	355	35	40.2	119	2	US-08-331-397B-46	Sequence 46, Appl
283	36	41.4	135	2	US-08-436-717-100	Sequence 100, App	356	35	40.2	119	2	US-08-759-804A-46	Sequence 46, Appl
284	36	41.4	135	2	US-08-436-717-102	Sequence 102, App	357	35	40.2	119	3	US-09-227-693-46	Sequence 46, Appl
285	36	41.4	135	2	US-08-436-717-112	Sequence 112, App	358	35	40.2	120	1	US-08-211-202-135	Sequence 135, App
286	36	41.4	135	2	US-08-860-174A-4	Sequence 4, Appl	359	35	40.2	120	1	US-07-942-245-35	Sequence 35, Appl
287	36	41.4	140	3	US-08-579-378A-4	Sequence 4, Appl	360	35	40.2	120	1	US-08-264-093-14	Sequence 14, Appl
288	36	41.4	140	3	US-08-579-378A-12	Sequence 12, Appl	361	35	40.2	120	4	US-09-513-999C-7802	Sequence 7802, Ap
289	36	41.4	140	5	PCT-US93-11612-4	Sequence 4, Appl	362	35	40.2	123	3	US-08-983-607-38	Sequence 38, Appl
290	36	41.4	140	5	PCT-US93-11612-12	Sequence 12, Appl	363	35	40.2	123	4	US-09-424-840B-16	Sequence 6, Appl
291	36	41.4	171	4	US-09-472-087-63	Sequence 83, Appl	364	35	40.2	124	1	US-08-276-852-126	Sequence 126, App
292	36	41.4	174	4	US-09-472-087-12	Sequence 12, Appl	365	35	40.2	124	1	US-08-899-575-126	Sequence 126, App
293	36	41.4	176	4	US-09-270-767-33791	Sequence 33791, A	366	35	40.2	124	1	US-08-899-575-126	Sequence 126, App
294	36	41.4	209	4	US-08-134-000C-5125	Sequence 5125, Ap	367	35	40.2	124	2	US-08-428-197-44	Sequence 44, Appl
295	36	41.4	212	2	US-08-737-129A-2	Sequence 2, Appl	368	35	40.2	124	4	US-09-424-840B-16	Sequence 16, Appl
296	36	41.4	229	4	US-09-107-532A-4842	Sequence 4842, Ap	369	35	40.2	124	5	PCT-US93-10555-44	Sequence 44, Appl
297	36	41.4	234	1	US-08-299-567-5	Sequence 5, Appl	370	35	40.2	124	5	PCT-US95-08743-126	Sequence 126, App
298	36	41.4	258	2	US-08-665-202-5	Sequence 5, Appl	371	35	40.2	126	4	US-09-599-360B-102	Sequence 102, App
299	36	41.4	258	4	US-09-315-574-5	Sequence 5, Appl	372	35	40.2	126	4	US-09-471-276-1559	Sequence 1559, Ap
300	36	41.4	262	3	US-09-069-821-4	Sequence 4, Appl	373	35	40.2	127	3	US-09-240-274-27	Sequence 27, Appl
301	36	41.4	262	4	US-09-956-086-4	Sequence 4, Appl	374	35	40.2	128	1	US-08-478-039-63	Sequence 63, Appl
302	36	41.4	262	4	US-09-956-087-4	Sequence 4, Appl	375	35	40.2	128	1	US-08-478-039-96	Sequence 96, Appl
303	36	41.4	274	2	US-08-860-174A-12	Sequence 12, Appl	376	35	40.2	128	1	US-08-476-349A-96	Sequence 96, Appl
304	36	41.4	274	4	US-09-248-796A-20856	Sequence 20856, A	377	35	40.2	128	1	US-08-476-349A-96	Sequence 96, Appl
305	36	41.4	282	3	US-09-420-592A-7	Sequence 7, Appl	378	35	40.2	129	4	US-09-615-192A-307	Sequence 307, App
306	36	41.4	282	4	US-09-985-442-7	Sequence 7, Appl	379	35	40.2	131	3	US-09-240-274-28	Sequence 28, Appl
307	36	41.4	282	4	US-09-983-580-7	Sequence 7, Appl	380	35	40.2	131	4	US-09-328-352-7719	Sequence 7719, Ap
308	36	41.4	292	3	US-09-372-422A-4	Sequence 4, Appl	381	35	40.2	139	4	US-08-454-899G-15	Sequence 15, Appl
309	36	41.4	301	4	US-09-902-540-13071	Sequence 13071, A	382	35	40.2	140	4	US-09-252-991A-22742	Sequence 22742, A
310	36	41.4	308	4	US-10-088-548-2	Sequence 2, Appl	383	35	40.2	141	4	US-09-489-039A-12648	Sequence 12648, A
311	36	41.4	309	4	US-09-248-796A-17217	Sequence 17217, A	384	35	40.2	144	4	US-09-489-039A-8229	Sequence 8229, Ap
312	36	41.4	397	4	US-09-489-039A-9401	Sequence 9401, Ap	385	35	40.2	155	4	US-09-252-991A-20803	Sequence 20803, A
313	36	41.4	446	4	US-09-902-540-13981	Sequence 13981, A	386	35	40.2	176	4	US-09-248-796A-21752	Sequence 21752, A
314	36	41.4	575	3	US-08-913-805A-10	Sequence 10, Appl	387	35	40.2	188	4	US-09-252-991A-24751	Sequence 24751, A
315	36	41.4	575	3	US-09-442-629-10	Sequence 10, Appl	388	35	40.2	213	3	US-08-630-820-6	Sequence 6, Appl
316	36	41.4	576	4	US-09-578-921A-2	Sequence 2, Appl	389	35	40.2	213	4	US-09-273-453-6	Sequence 6, Appl
317	36	41.4	827	4	US-09-134-000C-5747	Sequence 5747, Ap	390	35	40.2	229	4	US-09-107-532A-6876	Sequence 6876, Ap
318	36	41.4	943	3	US-09-397-885-5	Sequence 5, Appl	391	35	40.2	231	4	US-09-540-236-2087	Sequence 2087, Ap
319	36	41.4	943	4	US-09-969-362-5	Sequence 5, Appl	392	35	40.2	248	4	US-09-315-926A-80	Sequence 80, Appl

393 Sequence 83, Appl 3 US-09-188-579-83
394 Sequence 83, Appl 3 US-09-315-444-83
395 Sequence 83, Appl 3 US-09-721-362-83
396 Sequence 4, Appl 3 US-08-564-164A-4
397 Sequence 1, Appl 3 US-09-978-118-1
398 Sequence 33514, A 4 US-09-270-767-33514
399 Sequence 43648, A 4 US-09-270-767-43648
400 Sequence 43648, A 4 US-09-270-767-43648
401 Sequence 15052, A 3 US-08-628-796A-15052
402 Sequence 4, Appl 1 US-08-628-291-4
403 Sequence 4, Appl 2 US-09-128-722-4
404 Sequence 2, Appl 1 US-08-628-291-2
405 Sequence 2, Appl 2 US-09-128-722-2
406 Sequence 1, Appl 4 US-09-326-157-1
407 Sequence 1, Appl 4 US-10-135-755-1
408 Sequence 12, Appl 1 US-08-628-291-12
409 Sequence 12, Appl 2 US-09-128-722-12
410 Sequence 16, Appl 1 US-08-628-291-16
411 Sequence 16, Appl 2 US-09-128-722-16
412 Sequence 10573, A 4 US-09-949-016-10573
413 Sequence 14480, A 4 US-09-902-540-14480
414 Sequence 18974, A 4 US-09-248-796A-18974
415 Sequence 2, Appl 3 US-09-336-643A-2
416 Sequence 4, Appl 4 US-08-818-581B-4
417 Sequence 4, Appl 4 US-09-252-991A-28556
418 Sequence 24983, A 4 US-09-252-991A-24983
419 Sequence 5, Appl 4 US-09-828-995B-5
420 Sequence 29156, A 4 US-09-252-991A-29156
421 Sequence 10, Appl 4 US-08-487-596-10
422 Sequence 2, Appl 4 US-08-484-722-2
423 Sequence 10, Appl 4 US-08-660-451A-10
424 Sequence 9, Appl 3 US-08-881-784-9
425 Sequence 4, Appl 3 US-09-292-768-4
426 Sequence 68, Appl 3 US-09-292-768-68
427 Sequence 70, Appl 3 US-09-292-768-70
428 Sequence 14807, A 4 US-09-248-796A-14807
429 Sequence 4, Appl 4 US-09-919-172-4
430 Sequence 958, App 4 US-09-976-594-958
431 Sequence 11223, A 4 US-09-902-540-11223
432 Sequence 1194, App 4 US-09-538-092-1194
433 Sequence 15457, A 4 US-09-902-540-15457
434 Sequence 10, Appl 3 US-08-959-004-10
435 Sequence 25135, A 4 US-09-252-991A-25135
436 Sequence 489, App 4 US-09-976-594-489
437 Sequence 200, App 4 US-09-919-039-200
438 Sequence 25782, A 4 US-09-252-991A-25782
439 Sequence 5096, App 4 US-09-107-532A-5096
440 Sequence 11, Appl 1 US-08-220-603A-11
441 Sequence 40, Appl 3 US-08-485-355B-40
442 Sequence 41, Appl 4 US-09-865-621A-41
443 Sequence 72, Appl 4 US-09-661-596A-72
444 Sequence 5, Appl 1 US-08-489-733-5
445 Sequence 5, Appl 2 US-08-993-581B-5
446 Sequence 2, Appl 1 US-08-271-397-2
447 Sequence 2, Appl 3 US-08-469-191-2
448 Sequence 2, Appl 5 PCT-US91-07280-2
449 Sequence 7, Appl 28 US-09-388-890-7
450 Sequence 8, Appl 3 US-09-388-890-8
451 Sequence 1, Appl 28 US-09-264-709A-1
452 Sequence 7, Appl 28 US-09-660-954-7
453 Sequence 8, Appl 4 US-09-660-954-8
454 Sequence 85, Appl 3 US-08-676-124-95
455 Sequence 95, Appl 3 US-09-414-878-95
456 Sequence 95, Appl 3 US-09-240-136-95
457 Sequence 95, Appl 4 US-09-638-770A-95
458 Sequence 25580, A 4 US-09-248-796A-25580
459 Sequence 35678, A 4 US-09-270-767-35678
460 Sequence 50895, A 4 US-09-270-767-50895
461 Sequence 34248, A 4 US-09-270-767-34248
462 Sequence 49465, A 4 US-09-270-767-49465
463 Sequence 7147, App 4 US-09-513-999C-7147
464 Sequence 13, Appl 2 US-08-485-937-13
465 Sequence 13, Appl 2 US-08-373-215-13

466 Sequence 83, Appl 34 US-09-615-192A-267
467 Sequence 83, Appl 34 PCT-US93-08552-13
468 Sequence 83, Appl 34 US-09-270-767-39441
469 Sequence 4, Appl 34 US-08-270-767-54658
470 Sequence 1, Appl 34 US-08-230-592E-16
471 Sequence 33514, A 34 PCT-US95-10053-13
472 Sequence 43648, A 34 PCT-US96-09448-16
473 Sequence 43648, A 34 US-08-881-037-59
474 Sequence 15052, A 34 US-09-489-039A-8406
475 Sequence 4, Appl 34 US-08-341-843B-35
476 Sequence 4, Appl 34 US-08-427-497E-40
477 Sequence 2, Appl 34 US-08-602-787A-644
478 Sequence 2, Appl 34 US-08-793-490-9
479 Sequence 1, Appl 34 US-08-467-420A-15
480 Sequence 1, Appl 111 US-08-470-110A-15
481 Sequence 12, Appl 34 US-08-940-371-15
482 Sequence 12, Appl 2 US-08-881-037-14
483 Sequence 16, Appl 34 US-08-881-037-16
484 Sequence 16, Appl 34 US-08-637-647-15
485 Sequence 10573, A 34 US-08-273-146-59
486 Sequence 14480, A 34 US-09-726-219A-214
487 Sequence 18974, A 34 US-09-726-219A-222
488 Sequence 2, Appl 34 US-09-726-219A-225
489 Sequence 4, Appl 34 US-09-726-219A-233
490 Sequence 4, Appl 34 US-09-726-219A-234
491 Sequence 5, Appl 34 US-07-634-278-3
492 Sequence 24983, A 34 US-07-634-278-5
493 Sequence 29156, A 34 US-07-634-278-14
494 Sequence 10, Appl 34 US-08-477-728-3
495 Sequence 2, Appl 34 US-08-477-728-5
496 Sequence 10, Appl 34 US-08-477-728-5
497 Sequence 9, Appl 34 US-08-477-728-14
498 Sequence 68, Appl 34 US-08-474-040-3
499 Sequence 70, Appl 34 US-08-474-040-5
500 Sequence 14807, A 34 US-08-474-040-14

ALIGNMENTS

RESULT 1
US-08-370-156-25
; Sequence 25, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500

TELEFAX: (810) 689-4071
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-370-156-25

Query Match 100.0%; Score 87; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 Db 12 AEFHRWSSYVHWK 25

RESULT 2
 US-08-370-156-7
 ; Sequence 7, Application US/08370156
 ; Patent No. 5932780
 ; GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Zakut, Haim
 ; APPLICANT: Shani, Moshe
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
 ; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Reising, Ethington, Barnard & Perry
 ; STREET: P.O. Box 4390
 ; CITY: Troy
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48099
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,156
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 689-3500
 ; TELEFAX: (810) 689-4071
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-370-156-7

Query Match 100.0%; Score 87; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 Db 17 AEFHRWSSYVHWK 30

RESULT 3
 US-08-370-156-8
 ; Sequence 8, Application US/08370156
 ; Patent No. 5932780

GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Zakut, Haim
 ; APPLICANT: Shani, Moshe
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
 ; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Reising, Ethington, Barnard & Perry
 ; STREET: P.O. Box 4390
 ; CITY: Troy
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48099
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,156
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 689-3500
 ; TELEFAX: (810) 689-4071
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-370-156-8

Query Match 100.0%; Score 87; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 Db 17 AEFHRWSSYVHWK 30

RESULT 4
 US-08-990-065-21
 ; Sequence 21, Application US/08990065
 ; Patent No. 6121046
 ; GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Seidman, Shlomo
 ; APPLICANT: Eckstein, Fritz
 ; APPLICANT: Friedman, Alon
 ; APPLICANT: Kaufner, Daniela
 ; TITLE OF INVENTION: SYNTHETIC ANTISENSE
 ; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND PHARMACEUTICAL COMPOSITIONS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 6121046thwestern Hwy. Suite 410
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: U.S.
 ; ZIP: 48334
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/990,065
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/850,347
;; FILING DATE: 02-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,826
;; FILING DATE: 01-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Montgomery, Ilene N.
;; REGISTRATION NUMBER: 38,972
;; REFERENCE/DOCKET NUMBER: 2391.00086
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (248) 539-5050
;; TELEFAX: (248) 539-5055
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 45 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-990-065-21

Query Match 100.0%; Score 87; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVMVHWK 14
Db 17 AEFHRWSSYVMVHWK 30

RESULT 5
US-08-975-084-5
; Sequence 5, Application US/08975084
; Patent No. 6258780
; GENERAL INFORMATION:
; APPLICANT: SOREQ, Hermona
; APPLICANT: FRIEDMAN, Alon
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: KAUFER, Daniela
; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
; TITLE OF INVENTION: PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,084
; FILING DATE: 11-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-975-084-5

Query Match 100.0%; Score 87; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVMVHWK 14
Db 17 AEFHRWSSYVMVHWK 30

RESULT 6
US-09-380-532-11
; Sequence 11, Application US/09380532
; Patent No. 6475998
; GENERAL INFORMATION:
; APPLICANT: SOREQ, Hermona
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: SHOHAMI, Esther
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT OF INJURY TO THE CENTRAL NERVOUS SYSTEM
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6475998thwestern Hwy.
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,532
; FILING DATE: 12-No. 6475998-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00089
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-380-532-11

Query Match 100.0%; Score 87; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVMVHWK 14
Db 17 AEFHRWSSYVMVHWK 30

RESULT 7
US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-732-962A-2

Query Match 100.0%; Score 87; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 8
US-08-370-156-2
; Sequence 2, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-2

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 9
US-08-446-100-19
; Sequence 19, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE: human esterases
; ORGANISM: human esterases

US-08-446-100-19

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14

Db 586 AEFHRWSSYVHWK 599

RESULT 10

US-08-446-100-20
; Sequence 20, Application US/08446100

; Patent No. 6001625

; GENERAL INFORMATION:

; APPLICANT: Broomfield, Clarence A

; APPLICANT: Millard, Charles B

; APPLICANT: Lockridge, Oksana

; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hendricks and Assoc.

; STREET: 9669 A Main Street, P.O. Box 2509

; CITY: Fairfax

; STATE: VA

; COUNTRY: US

; ZIP: 22031

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,100

; FILING DATE: 19-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hendricks, Glenna

; REGISTRATION NUMBER: 32,535

; REFERENCE/DOCKET NUMBER: Broomfield

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 425-4250

; TELEFAX: (703) 425-2767

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 614 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ANTI-SENSE: YES

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: human esterases

US-08-446-100-20

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14

Db 586 AEFHRWSSYVHWK 599

RESULT 11

US-08-446-100-21

; Sequence 21, Application US/08446100

; Patent No. 6001625

; GENERAL INFORMATION:

; APPLICANT: Broomfield, Clarence A

; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hendricks and Assoc.

; STREET: 9669 A Main Street, P.O. Box 2509

; CITY: Fairfax

; STATE: VA

; COUNTRY: US

; ZIP: 22031

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,100

; FILING DATE: 19-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hendricks, Glenna

; REGISTRATION NUMBER: 32,535

; REFERENCE/DOCKET NUMBER: Broomfield

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 425-4250

; TELEFAX: (703) 425-2767

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 614 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ANTI-SENSE: YES

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: human esterases

US-08-446-100-21

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14

Db 586 AEFHRWSSYVHWK 599

RESULT 12

US-08-446-100-22

; Sequence 22, Application US/08446100

; Patent No. 6001625

; GENERAL INFORMATION:

; APPLICANT: Broomfield, Clarence A

; APPLICANT: Millard, Charles B

; APPLICANT: Lockridge, Oksana

; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hendricks and Assoc.

; STREET: 9669 A Main Street, P.O. Box 2509

; CITY: Fairfax

; STATE: VA

; COUNTRY: US

; ZIP: 22031

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-22

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 13
US-08-446-100-23
; Sequence 23, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Okaana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

```

```

; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-23

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 14
US-08-446-100-25
; Sequence 25, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Okaana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-25

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 15

```

```
US-08-814-095-2
; Sequence 2, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-814-095-2

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 16
PCT-US92-06106-2
; Sequence 2, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

US-09-949-016-7063
; Sequence 2, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7063
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7063

Query Match 100.0%; Score 87; DB 4; Length 645;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 617 AEFHRWSSYVHWK 630

RESULT 18
US-09-949-016-7064
; Sequence 2, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```



```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7064
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7064

Query Match      100.0%; Score 87; DB 4; Length 645;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSYVMVHWK 14
Db 617 AEFHRSSYVMVHWK 630

RESULT 19
US-08-348-920-1
; Sequence 1, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupandra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran
; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; TITLE OF INVENTION: Organophosphates
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-348-920-1

```

```

Query Match      92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred. No. 0.002;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRHSSYVMVHWK 14
Db 548 EFRHSSYVMVHWK 560

RESULT 20
US-08-348-920-2
; Sequence 2, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupandra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran
; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; TITLE OF INVENTION: Organophosphates
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-348-920-2

Query Match      92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred. No. 0.002;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRHSSYVMVHWK 14
Db 548 EFRHSSYVMVHWK 560

RESULT 21
5200183-5
; Patent No. 5200183
; APPLICANT: TANG, JORDAN J.N.;WANG, CHI-SUN
; TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
; NUMBER OF SEQUENCES: 22

```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,426
; FILING DATE: 12-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 504,635
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 122,410
; FILING DATE: 19-NOV-1987
; SEQ ID NO:5:
; LENGTH: 572
5200183-5
Query Match 71.3%; Score 62; DB 6; Length 572;
Best Local Similarity 64.3%; Pred. No. 0.56;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14
| | | | | : | |
Db 543 AGFHRWNNYMDWK 556

RESULT 22
5200183-5
; Patent No. 5200183
; APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
; TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,426
; FILING DATE: 12-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 504,635
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 122,410
; FILING DATE: 19-NOV-1987
; SEQ ID NO:5:
; LENGTH: 572
5200183-5
Query Match 71.3%; Score 62; DB 6; Length 572;
Best Local Similarity 64.3%; Pred. No. 0.56;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14
| | | | | : | |
Db 543 AGFHRWNNYMDWK 556

RESULT 23
5215909-12
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:12:
; LENGTH: 573
5215909-12
Query Match 71.3%; Score 62; DB 6; Length 573;
Best Local Similarity 64.3%; Pred. No. 0.56;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14
| | | | | : | |
Db 544 AGFHRWNNYMDWK 557
```

```
RESULT 24
5215909-12
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:12:
; LENGTH: 573
5215909-12
Query Match 71.3%; Score 62; DB 6; Length 573;
Best Local Similarity 64.3%; Pred. No. 0.56;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14
| | | | | : | |
Db 544 AGFHRWNNYMDWK 557

RESULT 25
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
```

```
; ORGANISM: human esterases
US-08-446-100-1
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 26
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-3

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 28
US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

; ORGANISM: human esterases
US-08-446-100-5
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 27
US-08-446-100-3
; Sequence 3, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-4

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 29
US-08-446-100-5
; Sequence 5, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-6

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 30
US-08-446-100-6
; Sequence 6, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-6

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586
```

```
;
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-5

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 30
US-08-446-100-6
; Sequence 6, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-6

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586
```

RESULT 31
US-08-446-100-7
; Sequence 7, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-7
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AEFHRWSSVMVHWK 14
Db 573 AGFHRWNNYMDWK 586
RESULT 32
US-08-446-100-8
; Sequence 8, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-8
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AEFHRWSSVMVHWK 14
Db 573 AGFHRWNNYMDWK 586
RESULT 33
US-08-446-100-9
; Sequence 9, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 9:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-9
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 34
US-08-446-100-10
; Sequence 10, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-10
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 35
US-08-446-100-11
; Sequence 11, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-11
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 36
US-08-446-100-12
; Sequence 12, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; US-08-446-100-12
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586
```

```

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 35
US-08-446-100-11
; Sequence 11, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-11
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586

RESULT 36
US-08-446-100-12
; Sequence 12, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; US-08-446-100-12
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 573 AGFHRWNNYMDWK 586
```

STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: human esterases
US-08-446-100-12

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : : : : :
Db 573 AGFHRWNNYMDWK 586

RESULT 37
US-08-446-100-13
Sequence 13, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Okeana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: human esterases
US-08-446-100-14

REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: human esterases
US-08-446-100-13

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : : : : :
Db 573 AGFHRWNNYMDWK 586

RESULT 38
US-08-446-100-14
Sequence 14, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Okeana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE: human esterases
US-08-446-100-14

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 39
US-08-446-100-15
; Sequence 15, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-15

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 40
US-08-446-100-16
; Sequence 16, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B

; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-16

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 41
US-08-446-100-17
; Sequence 17, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100

; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-17

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVMHWK 14
| | | | | : | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 42
US-08-446-100-18
; Sequence 18, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Okeana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-18

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVMHWK 14
| | | | | : | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 43
US-08-446-100-24
; Sequence 24, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Okeana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-24

Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVMHWK 14
| | | | | : | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 44
US-09-334-489-3

```
; Sequence 3, Application US/09334489
; Patent No. 6291175
; GENERAL INFORMATION:
; APPLICANT: Pierre Sevigny
; APPLICANT: Keith Schappert
; APPLICANT: Heiko Wiesbusch
; TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL
; DISEASE BY DETERMINING BCHE GENOTYPE
; FILE REFERENCE: 08523/013002
; CURRENT APPLICATION NUMBER: US/09/334,489
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 60/089,406
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-489-3
```

```
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 AEFHRWSSYVMVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586
```

```
RESULT 45
US-09-334-489-4
; Sequence 4, Application US/09334489
; Patent No. 6291175
; GENERAL INFORMATION:
; APPLICANT: Pierre Sevigny
; APPLICANT: Keith Schappert
; APPLICANT: Heiko Wiesbusch
; TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL
; DISEASE BY DETERMINING BCHE GENOTYPE
; FILE REFERENCE: 08523/013002
; CURRENT APPLICATION NUMBER: US/09/334,489
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 60/089,406
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-489-4
```

```
Query Match 71.3%; Score 62; DB 3; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.59;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 AEFHRWSSYVMVHWK 14
| | | | | : | |
Db 573 AGFHRWNNYMDWK 586
```

```
Search completed: October 12, 2005, 10:23:41
Job time : 46 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:06:29 ; Search time 56 Seconds

(without alignments)
128.020 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query- Match	Length	DB	ID	Description
1	87	100.0	39	2	Q9TSJ6	Q9TSJ6 bos taurus
2	87	100.0	526	2	Q86YX9	Q86YX9 homo sapien
3	87	100.0	584	1	ACES_RABIT	Q29499 oryctolagus
4	87	100.0	611	1	ACES_FELCA	Q62763 felis silve
5	87	100.0	613	1	ACES_BOVIN	P23795 bos taurus
6	87	100.0	614	1	ACES_HUMAN	P22303 homo sapien
7	87	100.0	614	1	ACES_MOUSE	P21836 mus musculus
8	87	100.0	614	1	ACES_RAT	P37136 rattus norv
9	87	100.0	614	2	Q67BC1	Q67BC1 macaca mula
10	84	96.6	633	1	ACES_ELEBEL	O42275 electrophor
11	80	92.0	95	2	Q9W6Y8	Q9W6Y8 torpedo cal
12	80	92.0	634	1	ACES_BRARE	Q86633 brachydanio
13	70	80.5	606	1	ACES_BUNFA	Q92035 bungarus fa
14	65	74.7	597	2	Q9JKC1	Q9JKC1 rattus norv
15	65	74.7	767	1	ACES_CHICK	P36196 gallus gall
16	62	71.3	64	2	Q96HL2	Q96HL2 homo sapien
17	62	71.3	574	1	CHLE_HORSE	P81908 equus cabal
18	62	71.3	602	1	CHLE_HUMAN	P62776 homo sapien
19	62	71.3	602	2	Q9N1N9	Q9N1N9 equus cabal
20	62	71.3	603	2	Q90ZK8	Q90ZK8 gallus gall
21	61	70.1	581	1	CHLE_RABIT	P21927 oryctolagus
22	61	70.1	603	1	CHLE_MOUSE	Q03311 mus musculus
23	56	64.4	602	1	CHLE_FELCA	Q82760 felis silve
24	56	64.4	602	1	CHLE_PANTT	Q82761 panthera ti
25	48	55.2	205	2	Q8B0J7	Q8B0J7 california
26	47	54.0	550	2	Q7RTL7	Q7RTL7 ciona savig
27	46.5	53.4	667	2	Q64NA7	Q64NA7 bacteroides
28	45	51.7	709	2	Q759Y3	Q759Y3 ashbya goss
29	44	50.6	143	2	Q857V6	Q857V6 mycobacteri
30	44	50.6	260	2	Q78318	Q78318 arabidopsis
31	44	50.6	328	2	Q8HRN8	Q8HRN8 arabidopsis

32	44	50.6	357	2	Q6YT37	Q6YT37 sus scrofa
33	44	50.6	467	1	Q7S6U0	Q7S6U0 neurospora
34	44	50.6	746	1	NUSC_ARATH	NUSC_ARATH arabidopsis
35	43.5	50.0	270	2	Q94BA9	Q94BA9 thagodia ba
36	43.5	50.0	651	2	Q89267	Q89267 bacteroides
37	43.5	50.0	692	2	Q8A059	Q8A059 bacteroides
38	43	49.4	186	2	Q7M2E7	Q7M2E7 photorhabdu
39	43	49.4	186	2	Q853E9	Q853E9 mycobacteri
40	43	49.4	223	2	Q96BH3	Q96BH3 homo sapien
41	43	49.4	223	2	Q96RT0	Q96RT0 homo sapien
42	43	49.4	392	2	Q9LWM9	Q9LWM9 arabidopsis
43	43	49.4	422	2	Q9LW89	Q9LW89 arabidopsis
44	43	49.4	516	1	SMP3_YEAST	SMP3_YEAST saccharomyc
45	43	49.4	564	2	Q95T11	Q95T11 drosophila
46	43	49.4	593	2	Q917D7	Q917D7 drosophila
47	43	49.4	2070	2	Q8KLL3	Q8KLL3 streptomyce
48	42	48.3	100	2	Q8ABN2	Q8ABN2 caulobacter
49	42	48.3	116	2	Q8WBV7	Q8WBV7 ostrinia nu
50	42	48.3	117	2	Q8WB28	Q8WB28 ostrinia fu
51	42	48.3	138	2	Q8P335	Q8P335 xanthomonas
52	42	48.3	138	2	Q8PKN2	Q8PKN2 xanthomonas
53	42	48.3	143	2	Q8FRL6	Q8FRL6 corynebacte
54	42	48.3	150	2	Q8PRG8	Q8PRG8 xanthomonas
55	42	48.3	261	2	Q9GL26	Q9GL26 canis famli
56	42	48.3	322	2	Q6DSE9	Q6DSE9 erwinia car
57	42	48.3	553	2	Q7SXB7	Q7SXB7 brachydanio
58	42	48.3	558	2	Q99XQ8	Q99XQ8 mus musculu
59	42	48.3	657	2	Q9UUD3	Q9UUD3 orpinomyces
60	42	48.3	657	2	Q9GDW2	Q9GDW2 emilax hlep
61	42	48.3	664	2	Q9C122	Q9C122 piromyces s
62	42	48.3	723	2	Q89YE5	Q89YE5 bradyrhizob
63	42	48.3	755	2	Q659E9	Q659E9 homo sapien
64	42	48.3	768	2	Q64UC7	Q64UC7 bacteroides
65	42	48.3	822	1	ANC2_HUMAN	ANC2_HUMAN homo sapien
66	42	48.3	837	1	ANC2_MOUSE	ANC2_MOUSE mus musculu
67	42	48.3	838	2	Q6ZPR8	Q6ZPR8 mus musculu
68	42	48.3	1084	2	Q9H1R7	Q9H1R7 homo sapien
69	42	48.3	1103	2	Q7TWMJ2	Q7TWMJ2 mus musculu
70	42	48.3	1788	2	Q60611	Q60611 homo sapien
71	42	48.3	1788	2	Q60612	Q60612 homo sapien
72	42	48.3	1792	2	Q46385	Q46385 bos taurus
73	42	48.3	2031	2	Q8K4L2	Q8K4L2 mus musculu
74	42	48.3	2073	2	Q6UIJ6	Q6UIJ6 mustela put
75	42	48.3	2170	2	Q8K4L3	Q8K4L3 mus musculu
76	42	48.3	2214	2	Q95425	Q95425 homo sapien
77	41.5	47.7	133	2	Q6D801	Q6D801 erwinia car
78	41	47.1	117	2	Q94XC9	Q94XC9 caecilius q
79	41	47.1	145	2	Q675X0	Q675X0 oikopleura
80	41	47.1	153	2	Q98HQ0	Q98HQ0 rhizobium l
81	41	47.1	177	2	Q9RMA7	Q9RMA7 bacillus ci
82	41	47.1	220	2	Q9NNQ6	Q9NNQ6 homo sapien
83	41	47.1	230	2	Q8GVB4	Q8GVB4 leucojum ae
84	41	47.1	237	2	Q62GB7	Q62GB7 burkholderi
85	41	47.1	237	2	Q63065	Q63065 burkholderi
86	41	47.1	242	2	Q8GVA9	Q8GVA9 acis nicaee
87	41	47.1	250	2	Q8GVA4	Q8GVA4 acis valent
88	41	47.1	250	2	Q8GVB3	Q8GVB3 acis autumn
89	41	47.1	289	2	Q6MLZ2	Q6MLZ2 bdellovibri
90	41	47.1	397	2	Q9V095	Q9V095 pyrococcus
91	41	47.1	398	2	Q98618	Q98618 rhizobium l
92	41	47.1	408	2	Q8TH21	Q8TH21 pyrococcus
93	41	47.1	414	2	Q9UM44	Q9UM44 homo sapien
94	41	47.1	468	2	Q8R157	Q8R157 mus musculu
95	41	47.1	477	2	Q9TMK2	Q9TMK2 galanthus e
96	41	47.1	477	2	Q8M904	Q8M904 stylidium b
97	41	47.1	499	2	Q8DHN3	Q8DHN3 synechococc
98	41	47.1	509	2	Q9FNY9	Q9FNY9 arabidopsis
99	41	47.1	512	2	Q9C8X2	Q9C8X2 arabidopsis
100	41	47.1	516	2	Q8GV94	Q8GV94 galanthus n

105	41	47.1	520	2	Q8GV99	Q8gv99 galanthus f	178	40	46.0	378	2	Q9TMC2	Q9tmg2 crocus sati
106	41	47.1	520	2	Q8GVA0	Q8gva0 galanthus e	179	40	46.0	450	2	Q25000	Q25000 helicobacte
107	41	47.1	520	2	Q8GVA1	Q8gva1 galanthus c	180	40	46.0	453	2	Q6UVW8	Q6uvw8 homo sapien
108	41	47.1	520	2	Q8GVA2	Q8gva2 galanthus a	181	40	46.0	517	2	Q9XPP6	Q9xpp6 pseudotrill
109	41	47.1	520	2	Q8GVA5	Q8gva5 acis valent	182	40	46.0	520	2	Q8GV95	Q8gv95 galanthus l
110	41	47.1	520	2	Q8GV82	Q8gv82 acis autumn	183	40	46.0	521	2	Q877D5	Q877d5 pyroabacul
111	41	47.1	520	2	Q8GV85	Q8gv85 leucomum ae	184	40	46.0	534	2	Q72WN9	Q72wn9 xenopus lae
112	41	47.1	523	2	Q87GW8	Q87gw8 clostridium	185	40	46.0	540	2	Q870B7	Q870b7 piromyces s
113	41	47.1	527	2	Q8GDM1	Q8gdm1 photorhabdu	186	40	46.0	540	2	Q870B7	Q870b7 piromyces s
114	41	47.1	527	2	Q8KAJ7	Q8ka7 bacillus ha	187	40	46.0	586	2	Q74IP7	Q74ip7 lactobacill
115	41	47.1	535	2	Q8SEV8	Q8sev8 neurospora	188	40	46.0	606	2	Q8REH6	Q8reh6 fusobacteri
116	41	47.1	694	2	Q8SEV8	Q8sev8 neurospora	188	40	46.0	650	2	Q7RZT5	Q7rzt5 neurospora
117	41	47.1	818	2	Q9KB88	Q9kb88 bacillus ha	189	40	46.0	658	2	Q870B6	Q870b6 androcymbi
118	41	47.1	1155	2	Q6TKT8	Q6tk8 escherichia	190	40	46.0	665	2	Q870B6	Q870b6 piromyces s
119	41	47.1	1181	2	Q8GDM1	Q8gdm1 photorhabdu	191	40	46.0	678	2	Q716T9	Q716t9 kreysigia s
120	41	47.1	1243	2	Q8GQT8	Q8gqt8 mus musculu	192	40	46.0	690	2	Q716T9	Q716t9 kreysigia s
121	41	47.1	1252	2	Q8BLU9	Q8blu9 leishmania	193	40	46.0	707	2	Q8NEE6	Q8nee6 homo sapien
122	41	47.1	1261	2	Q90ZWS	Q90zws gallus gall	194	40	46.0	716	1	Q8NEE6	Q8nee6 homo sapien
123	41	47.1	1323	1	SAL3_MOUSE	Q62255 mus musculu	195	40	46.0	731	2	RRP2_IALTE	RRP2 influenza a
124	41	47.1	1687	2	Q7F8R6	Q7f8r6 oryza sati	196	40	46.0	736	2	Q6TMMX8	Q6tmx8 schistosoma
125	40.5	46.6	160	2	Q834V9	Q834v3 geobacter s	197	40	46.0	736	2	Q8N7Y4	Q8n7y4 homo sapien
126	40.5	46.6	175	2	Q8BS90	Q8bs90 enterococcu	198	40	46.0	740	2	Q6TMY2	Q6tm2 schistosoma
127	40.5	46.6	212	2	Q6BS89	Q6bs89 debaryomyce	199	40	46.0	749	2	Q6TMY0	Q6tm0 schistosoma
128	40.5	46.6	265	2	Q94BB9	Q94bb9 plinthus cr	201	40	46.0	844	2	Q7V511	Q7v511 prochloroco
129	40.5	46.6	269	2	Q719D8	Q719d8 silene nuta	202	40	46.0	844	2	Q8IG87	Q8ig87 drosophila
130	40.5	46.6	269	2	Q94BB9	Q94bb9 silene roth	203	40	46.0	1179	2	Q8S9X1	Q8s9x1 oryza sati
131	40.5	46.6	270	2	Q94BB5	Q94bb5 portulacaci	204	40	46.0	1350	2	Q9N8M4	Q9n8m4 trypanosoma
132	40.5	46.6	271	2	Q94BB3	Q94bb3 galenia pub	205	40	46.0	1784	2	Q9VE54	Q9ve54 drosophila
133	40.5	46.6	274	2	Q94BK1	Q94bk1 axyris hydr	206	39.5	45.4	1995	1	YCX7_CHLRE	YCX7 chlamydomon
134	40.5	46.6	276	2	Q94BF0	Q94bf0 honckenia p	207	39.5	45.4	198	2	Q7NDG5	Q7ndg5 gloeobacter
135	40.5	46.6	277	2	Q94BL4	Q94bl4 agdestis cl	208	39.5	45.4	276	2	Q6R1V7	Q6r1v7 sapranthus
136	40.5	46.6	277	2	Q94BL4	Q94bl4 agdestis cl	209	39.5	45.4	276	2	Q6R1X7	Q6r1x1 polyalthia
137	40.5	46.6	278	2	Q94BL9	Q94bl9 achatocarpu	210	39.5	45.4	276	2	Q6R1X2	Q6r1x2 polyalthia
138	40.5	46.6	280	2	Q94BC1	Q94bc1 phytolacca	211	39.5	45.4	276	2	Q6R1X3	Q6r1x3 polyalthia
139	40.5	46.6	280	2	Q94BH6	Q94bh6 didierea tr	212	39.5	45.4	276	2	Q6R1X4	Q6r1x4 enicoeanthu
140	40.5	46.6	281	2	Q94BC0	Q94bc0 pisonia umb	213	39.5	45.4	276	2	Q6R1X6	Q6r1x6 enicoeanthu
141	40.5	46.6	281	2	Q94BC8	Q94bc8 oxybaphus n	214	39.5	45.4	276	2	Q6R1X7	Q6r1x7 polyalthia
142	40.5	46.6	281	2	Q94BH8	Q94bh8 decarya mad	215	39.5	45.4	276	2	Q6R1X8	Q6r1x8 polyalthia
143	40.5	46.6	283	2	Q94BL1	Q94bl1 alluandia a	216	39.5	45.4	276	2	Q6R1X9	Q6r1x9 polyalthia
144	40.5	46.6	285	2	Q94BC2	Q94bc2 phaulothamn	217	39.5	45.4	276	2	Q6R1Y0	Q6r1y0 polyalthia
145	40.5	46.6	285	2	Q94B19	Q94b19 calyptroche	218	39.5	45.4	276	2	Q6R1Y1	Q6r1y1 polyalthia
146	40.5	46.6	289	2	Q94BF9	Q94bf9 gliostroche	219	39.5	45.4	429	2	Q6R1Y2	Q6r1y2 polyalthia
147	40.5	46.6	293	2	Q94BL0	Q94bl0 alluandiops	220	39.5	45.4	435	2	Q9GG33	Q9gg33 limnobiolum l
148	40.5	46.6	442	2	Q9L1F1	Q9l1f1 streptomyce	221	39.5	45.4	440	2	Q9GG34	Q9gg34 lagarosiphon
149	40.5	46.6	469	2	Q7NX74	Q7nx74 chromobacte	222	39.5	45.4	447	2	Q7Z4R4	Q7z4r4 homo sapien
150	40.5	46.6	502	2	Q98DL0	Q98dl0 rhizobium l	223	39.5	45.4	469	2	Q6ZMD5	Q6zmd5 homo sapien
151	40.5	46.6	508	2	Q78332	Q78332 perularia	224	39.5	45.4	469	2	P73738	P73738 synechocyst
152	40.5	46.6	510	1	AC01_YEAST	P21147 saccharomyc	225	39.5	45.4	470	2	Q6GDT2	Q6gdt2 staphylococ
153	40.5	46.6	510	2	Q6B1S0	Q6bls0 saccharomyc	226	39.5	45.4	494	2	Q7UB36	Q7ub36 shigella fl
154	40.5	46.6	511	2	Q78334	Q78334 tylophora i	227	39.5	45.4	497	2	Q83PI3	Q83pi3 shigella fl
155	40.5	46.6	511	2	Q78335	Q78335 vincetoxicu	228	39.5	45.4	498	2	Q6C2D8	Q6czd8 erwinia car
156	40.5	46.6	1052	2	Q7QB12	Q7qb12 anophales g	229	39.5	45.4	507	2	Q717Z2	Q717z2 annonia muri
157	40	46.0	67	2	Q8EE00	Q8ee00 shewanella	230	39.5	45.4	509	2	Q7YKL8	Q7ykl8 genlisea ro
158	40	46.0	136	2	Q6YIF6	Q6yif6 oryza sati	231	39.5	45.4	510	2	Q7YKML	Q7ykm1 genlisea au
159	40	46.0	183	2	Q57000	Q57000 zymomonas m	232	39.5	45.4	512	2	Q78333	Q78333 pentarrhinu
160	40	46.0	211	2	Q9K8C4	Q9k8c4 bacillus ha	233	39.5	45.4	542	2	Q64858	Q64858 arabidopsis
161	40	46.0	218	2	Q8GV90	Q8gv90 galanthus r	234	39.5	45.4	611	2	Q96PB9	Q96pb9 homo sapien
162	40	46.0	232	2	Q8GVA8	Q8gva8 acis rosea	235	39.5	45.4	611	2	Q9H068	Q9h068 homo sapien
163	40	46.0	243	2	Q8W5L5	Q8w5l5 oryza sati	236	39.5	45.4	618	2	Q96GS7	Q96gs7 homo sapien
164	40	46.0	243	2	Q7XH69	Q7xh69 oryza sati	237	39.5	45.4	618	2	Q9H6U8	Q9h6u8 homo sapien
165	40	46.0	245	1	YG24_YEAST	P53237 saccharomyc	238	39.5	45.4	699	2	Q9F9J5	Q9f9j5 sulfolobus
166	40	46.0	249	1	UBIE_LEPIN	Q8exj3 leptospira	239	39.5	45.4	1057	2	Q9Y8H1	Q9y8h1 tricholoma
167	40	46.0	249	2	Q75FL1	Q75fl1 leptospira	240	39.5	45.4	1198	2	Q6FPG4	Q6fpg4 candida gla
168	40	46.0	268	2	Q94B13	Q94b13 claytonia m	241	39	44.8	48	2	Q85KI0	Q85ki0 trissolcus
169	40	46.0	271	2	Q94BF1	Q94bf1 hilleria la	242	39	44.8	100	2	Q23949	Q23949 gossypium h
170	40	46.0	274	2	Q94B98	Q94b98 segueria a	243	39	44.8	116	2	Q8SEY7	Q8sey7 bombyx mori
171	40	46.0	283	2	Q94BD6	Q94bd6 montia parv	244	39	44.8	116	2	Q9MIE8	Q9mie8 bombyx mand
172	40	46.0	303	2	Q82R18	Q82r18 streptomyce	245	39	44.8	138	1	Q6JVA0	Q6jva0 mus musculu
173	40	46.0	314	2	Q7PVC5	Q7pvc6 anophales g	246	39	44.8	143	2	Q69SG2	Q69sg2 oryza sati
174	40	46.0	330	2	Q8HR50	Q8hr50 cadaba virg	247	39	44.8	150	2	Q6YBA2	Q6yba2 staphylococ
175	40	46.0	330	2	Q8HR51	Q8hr51 cadaba kirk	248	39	44.8	150	2	Q5YBA3	Q5yba3 staphylococ
176	40	46.0	351	2	Q72754	Q72754 cowpox viru	249	39	44.8	150	2	Q6YBA4	Q6yba4 staphylococ
177	40	46.0	355	2	Q87H15	Q87hl5 vibrio para	250	39	44.8	150	2	Q6YBA6	Q6yba6 staphylococ

251	39	44.8	150	2	Q6YBA8	Q5yba8 staphylococ	324	39	44.8	542	2	Q7TPQ2	Q7tpq2 mus musculu
252	39	44.8	150	2	Q6YB80	Q5ybb0 staphylococ	325	39	44.8	575	1	UL87_EBV	P25215 epstein-bar
253	39	44.8	151	2	Q8NSG0	Q8nsg0 corynebacte	326	39	44.8	644	1	PSAB_AMPCA	P58393 amphidinim
254	39	44.8	155	2	Q9K2H1	Q9k2h1 staphylococ	327	39	44.8	651	2	Q8NYB1	Q8nyb1 staphylococ
255	39	44.8	155	2	Q9K2M4	Q9k2m4 staphylococ	328	39	44.8	651	2	Q832J5	Q832j5 staphylococ
256	39	44.8	155	2	Q9L3Y9	Q9l3y9 staphylococ	329	39	44.8	651	2	Q99WP4	Q99wp4 staphylococ
257	39	44.8	155	2	Q9L3Z0	Q9l3z0 staphylococ	330	39	44.8	651	2	Q6GCD9	Q6gcd9 staphylococ
258	39	44.8	155	2	Q9L3Z1	Q9l3z1 staphylococ	331	39	44.8	651	2	Q6GJY4	Q6ggy4 staphylococ
259	39	44.8	155	2	Q9L3Z2	Q9l3z2 staphylococ	332	39	44.8	654	2	Q70G41	Q70g41 amphidinim
260	39	44.8	157	2	Q84B73	Q84b73 vibrio natr	333	39	44.8	656	2	Q9GDX8	Q9gdx8 clintonia b
261	39	44.8	157	2	Q8GFP1	Q8gfh1 vibrio pela	334	39	44.8	660	2	Q9GDX1	Q9gdx1 notholirion
262	39	44.8	157	2	Q87NK2	Q87nk2 vibrio para	335	39	44.8	667	2	Q7UM38	Q7um38 rhodopirell
263	39	44.8	166	2	Q8D5M2	Q8d5m2 vibrio vuln	336	39	44.8	690	2	Q6EMT9	Q6em9 marantochlo
264	39	44.8	168	2	Q6FB16	Q6fb16 acinetobact	337	39	44.8	750	2	Q8AZJ6	Q8azj6 human herpe
265	39	44.8	170	2	Q7V9Z1	Q7v9z1 prochloroco	338	39	44.8	866	2	Q6UEQ7	Q6ueq7 human immun
266	39	44.8	199	2	Q9KUL9	Q9kul9 vibrio chol	339	39	44.8	945	2	Q6CYB0	Q6cyb0 kluyveromyc
267	39	44.8	213	2	Q7RZ07	Q7rz07 neurospora	340	39	44.8	1060	2	Q7UKA3	Q7uka3 rhodopirell
268	39	44.8	223	2	Q871E2	Q871e2 neurospora	341	39	44.8	1237	1	YD2_SCHPO	O13663 achizosacch
269	39	44.8	226	1	VNE1_PEDV7	P59771 porcine epi	342	39	44.8	1300	1	SAL3_HUMAN	Q9bxa9 homo sapien
270	39	44.8	226	1	VNE1_PEDV8	P59770 porcine epi	343	39	44.8	1368	2	Q9NS31	Q9ns31 caenorhabdi
271	39	44.8	226	2	C37049	O37049 porcine epi	344	39	44.8	1401	2	Q9NS30	Q9ns30 caenorhabdi
272	39	44.8	226	2	C37351	O37351 porcine epi	345	39	44.8	1679	2	Q7Q7K8	Q7q7k8 anopheles g
273	39	44.8	226	2	Q72839	Q72839 porcine epi	346	38.5	44.3	177	2	Q7Q782	Q7q782 anopheles g
274	39	44.8	226	2	Q91AU9	Q91au9 porcine epi	347	38.5	44.3	185	2	Q7PDX1	Q7pdx1 anopheles g
275	39	44.8	226	2	Q892M0	Q892m0 porcine epi	348	38.5	44.3	196	2	Q8YQY7	Q8yqy7 anabaena sp
276	39	44.8	226	2	Q6J0S8	Q6j0s8 porcine epi	349	38.5	44.3	204	2	Q8ZNS6	Q8zns6 streptomyce
277	39	44.8	230	2	Q91E21	Q91ez1 cydia pomon	350	38.5	44.3	269	2	Q8WI39	Q8wi39 dioscorea c
278	39	44.8	240	2	Q811R5	Q811r5 bacillus ce	351	38.5	44.3	270	2	Q8CQ43	Q8cq43 staphylococ
279	39	44.8	259	2	Q78312	Q78312 sisymbrium	352	38.5	44.3	275	2	Q94B73	Q94b73 bosea cypr
280	39	44.8	260	2	Q78311	Q78311 brassica ol	353	38.5	44.3	277	2	Q932F3	Q932f3 staphylococ
281	39	44.8	260	2	Q78313	Q78313 stanleya pi	354	38.5	44.3	277	2	Q99VX8	Q99vx8 staphylococ
282	39	44.8	260	2	Q78320	Q78320 thiaepi arv	355	38.5	44.3	277	2	Q7AIM3	Q7aim3 staphylococ
283	39	44.8	262	2	O10441	O10441 mouse adeno	356	38.5	44.3	277	2	Q6GBJ2	Q6gbj2 staphylococ
284	39	44.8	266	2	Q93HH2	Q93hh2 streptomyce	357	38.5	44.3	277	2	Q6GJ32	Q6gj32 staphylococ
285	39	44.8	272	2	Q99UH4	Q99uh4 staphylococ	358	38.5	44.3	280	2	Q94BB4	Q94bb4 psilotrichu
286	39	44.8	272	2	Q7A106	Q7a106 staphylococ	359	38.5	44.3	283	2	Q94BD7	Q94bd7 moehringia
287	39	44.8	272	2	Q7A5V8	Q7a5v8 staphylococ	360	38.5	44.3	287	1	XT14_ARATH	Q2zsu4 arabidopsis
288	39	44.8	272	2	Q6G9R4	Q6g9r4 staphylococ	361	38.5	44.3	354	2	Q98848	Q98848 cornus cana
289	39	44.8	272	2	Q6GHD6	Q6ghd6 staphylococ	362	38.5	44.3	395	2	Q7UXA8	Q7uxa8 rhodopirell
290	39	44.8	274	2	Q896N4	Q896n4 clostridium	363	38.5	44.3	499	2	Q9CJZ0	Q9cjz0 pasteurella
291	39	44.8	274	2	Q8CP87	Q8cp87 staphylococ	364	38.5	44.3	517	2	Q9GHB5	Q9ghb5 dioscorea a
292	39	44.8	277	2	Q9FYE3	Q9fye3 arabidopsis	365	38.5	44.3	613	2	Q940E7	Q940e7 agastache r
293	39	44.8	280	2	Q94BL3	Q94bl3 agrostemma	366	38.5	44.3	620	2	Q9FWU5	Q9fwu5 echinonetet
294	39	44.8	298	2	Q7SKV5	Q7skv5 brachydanio	367	38.5	44.3	907	2	Q8YZ60	Q8yz60 anabaena sp
295	39	44.8	299	2	Q67VG2	Q67vg2 oryza sativ	368	38	43.7	35	2	Q8SG47	Q8sg47 gastrophil
296	39	44.8	299	2	Q6ANU8	Q6anj8 desulfotale	369	38	43.7	43	2	Q8SG43	Q8sg43 cf. senosto
297	39	44.8	308	2	Q7XDX0	Q7xdx0 oryza sativ	370	38	43.7	50	2	Q8SG61	Q8sg61 ectinorhync
298	39	44.8	318	2	Q6A7W9	Q6a7w9 propionibac	371	38	43.7	56	2	Q98928	Q98928 gallus gall
299	39	44.8	328	2	Q8HRN1	Q8hrn1 stanleya pi	372	38	43.7	82	2	Q6B854	Q6b854 meriones un
300	39	44.8	328	2	Q8HRN2	Q8hrn2 sisymbrium	373	38	43.7	117	1	NU3M_DROME	P18930 drosophila
301	39	44.8	335	2	Q9L610	Q9l610 thiocapsa r	374	38	43.7	117	1	NU3M_DROU	P51940 drosophila
302	39	44.8	342	2	Q9L1H0	Q9l1h0 triglochcin	375	38	43.7	117	1	NU3M_DROYA	P07705 drosophila
303	39	44.8	357	2	Q6N2K6	Q6n2k6 rhodopseudo	376	38	43.7	117	2	Q6XSI5	Q6xsl5 bactrocera
304	39	44.8	357	2	Q89HMS	Q89hms bradyrhizob	377	38	43.7	117	2	Q7IV53	Q7iv53 drosophila
305	39	44.8	374	2	Q654H0	Q654h0 oryza sativ	378	38	43.7	117	2	Q9MD67	Q9md67 drosophila
306	39	44.8	376	2	Q6Q211	Q6q211 hyposter f	379	38	43.7	117	2	Q9MDN9	Q9mdn9 drosophila
307	39	44.8	394	2	Q8A2D1	Q8a2d1 bacteroides	380	38	43.7	117	2	Q9MGL2	Q9mgl2 drosophila
308	39	44.8	400	2	Q67VG3	Q67vg3 oryza sativ	381	38	43.7	117	2	Q9MGL9	Q9mgl9 drosophila
309	39	44.8	401	2	Q8RUP6	Q8rup6 oryza sativ	382	38	43.7	117	2	Q9MGM8	Q9mgm8 drosophila
310	39	44.8	408	2	Q9HXZ9	Q9hxz9 pseudomonas	383	38	43.7	117	2	Q9XMN6	Q9xmnm6 ceratitis c
311	39	44.8	422	2	Q8EH43	Q8eh43 shewanella	384	38	43.7	118	2	Q9BZU0	Q9bzj0 chrysomya p
312	39	44.8	441	2	O15814	O15814 dictyosteli	385	38	43.7	118	2	Q9MPF4	Q9mpf4 cochlomyia
313	39	44.8	444	2	Q8PF64	Q8pf64 xanthomonas	386	38	43.7	137	2	Q71IR9	Q71ir9 lactobacill
314	39	44.8	451	2	Q7QL14	Q7ql14 anopheles g	387	38	43.7	157	2	Q9KSE7	Q9kse7 vibrio chol
315	39	44.8	498	2	Q6LA25	Q6la25 triglochcin	388	38	43.7	162	2	Q7Q8F5	Q7q8f5 anopheles g
316	39	44.8	500	2	Q7Y1V8	Q7yiv8 zosteria cae	389	38	43.7	181	2	Q64AE2	Q64ae2 uncultured
317	39	44.8	506	2	Q9GHB4	Q9ghb4 freycinetia	390	38	43.7	181	2	Q64DV1	Q64dv1 uncultured
318	39	44.8	507	1	SXA2_SCHPO	P32825 schizosacch	391	38	43.7	184	2	Q648T9	Q648t9 uncultured
319	39	44.8	513	2	Q7XC43	Q7xc43 oryza sativ	392	38	43.7	184	2	Q64AW6	Q64aw6 uncultured
320	39	44.8	513	2	Q9AY56	Q9ay56 oryza sativ	393	38	43.7	193	1	NADD_BRAJA	Q89x84 bradyrhizob
321	39	44.8	524	2	O49650	O49650 arabidopsis	394	38	43.7	203	2	Q9U0N3	Q9u0n3 plasmodium
322	39	44.8	524	2	Q93ZX2	Q93zx2 arabidopsis	395	38	43.7	209	2	Q6NBE3	Q6nde3 rhodopseudo
323	39	44.8	526	2	O49652	O49652 arabidopsis	396	38	43.7	210	2	Q6VF40	Q6vf40 pipa parva

397	38	43.7	218	2	Q701X8	Q7qlx8 anopheles g
398	38	43.7	234	2	Q6J345	Q6j345 vaccinia vi
399	38	43.7	237	2	Q97UG9	Q97ug9 sulfolobus
400	38	43.7	239	2	Q7VJ29	Q7vj29 helicobacte
401	38	43.7	239	2	Q8UJ27	Q8uj27 agrobacteri
402	38	43.7	240	2	Q9VR89	Q9vr89 drosophila
403	38	43.7	245	2	Q9GL25	Q9gl25 canis famil
404	38	43.7	247	2	Q88EQ6	Q88eq6 pseudomonas
405	38	43.7	247	2	Q88EQ6	Q88eq6 pseudomonas
406	38	43.7	250	2	Q73TH3	Q73th3 mycobacteri
407	38	43.7	255	2	Q8XP77	Q8xp77 clostridium
408	38	43.7	265	2	Q7Q1X7	Q7qlx7 anopheles g
409	38	43.7	267	1	Q9DUN2	Q9dun2 vaccinia vi
410	38	43.7	267	1	TJ32_ARATH	O22588 arabidopsis
411	38	43.7	279	2	Q675A4	Q675a4 physcomitre
412	38	43.7	280	2	Q815Q4	Q815q4 plasmodium
413	38	43.7	283	2	Q6FMX7	Q6fmx7 candida gla
414	38	43.7	286	2	Q67PH1	Q67ph1 symbiobacte
415	38	43.7	292	2	Q97737	Q97737 bos taurus
416	38	43.7	295	1	Y770_MYCTU	P71825 mycobacteri
417	38	43.7	295	2	Q7U1B4	Q7ulb4 mycobacteri
418	38	43.7	298	2	Q828J2	Q828j2 salmonella
419	38	43.7	298	2	Q82R14	Q82r14 salmonella
420	38	43.7	302	2	Q92YK3	Q92yk3 rhizobium m
421	38	43.7	313	2	Q8FUV7	Q8fuv7 methanosarc
422	38	43.7	314	2	Q97AD4	Q97ad4 thermoplasma
423	38	43.7	321	2	Q91FU7	Q91fu7 bean 58058
424	38	43.7	321	2	Q63XT9	Q63xt9 burkholderi
425	38	43.7	324	2	Q654H2	Q654h2 oryza sativ
426	38	43.7	324	2	Q9JJ84	Q9jj84 rattus norv
427	38	43.7	340	2	Q7V0U9	Q7v0u9 prochloroco
428	38	43.7	342	2	Q96105	Q96105 homo sapien
429	38	43.7	351	1	VB19_VACCD	P23998 vaccinia vi
430	38	43.7	351	1	VB19_VACCV	P25213 vaccinia vi
431	38	43.7	351	2	Q6RZB2	Q6rzb2 rabbitpox v
432	38	43.7	351	2	Q76ZK5	Q76zk5 vaccinia vi
433	38	43.7	352	2	Q8V4R2	Q8v4r2 monkeypox v
434	38	43.7	353	1	VB19_VACCC	P21077 vaccinia vi
435	38	43.7	353	2	Q6RFI1	Q6rfi1 vaccinia vi
436	38	43.7	353	2	Q9JF34	Q9jf34 vaccinia vi
437	38	43.7	355	2	Q6RFI2	Q6rfi2 cartagalo o
438	38	43.7	356	2	Q8WKY7	Q8wky7 arctostaphy
439	38	43.7	358	2	Q928M1	Q928m1 listeria in
440	38	43.7	364	2	Q9FY29	Q9fy29 antirrhinum
441	38	43.7	366	2	Q8QMN5	Q8qmn5 cowpox viru
442	38	43.7	379	2	O44791	O44791 caenorhabdi
443	38	43.7	379	2	Q9TM11	Q9tm11 agapanthus
444	38	43.7	380	2	Q8DPT8	Q8dpt8 vibrio vuln
445	38	43.7	388	2	Q8LSQ2	Q8lsq2 oryza sativ
446	38	43.7	399	2	Q7MPY8	Q7mpy8 vibrio vuln
447	38	43.7	413	2	Q8NBB7	Q8nbb7 homo sapien
448	38	43.7	419	2	Q72E86	Q72e86 desulfovibr
449	38	43.7	422	2	Q9IMS8	Q9ims8 cherry mott
450	38	43.7	455	2	Q7NMJ4	Q7nmj4 vibrio vuln
451	38	43.7	455	2	Q8DGO1	Q8dgo1 vibrio vuln
452	38	43.7	468	2	Q880W3	Q880w3 pseudomonas
453	38	43.7	474	2	P93717	P93717 petunia hyb
454	38	43.7	478	2	Q8W3P8	Q8w3p8 phaseolus a
455	38	43.7	497	2	Q62BJ2	Q62bj2 burkholderi
456	38	43.7	497	2	Q63LV1	Q63lv1 burkholderi
457	38	43.7	511	2	Q9GNG8	Q9gng8 acorus gram
458	38	43.7	515	1	MATK_TRION	Q9xpp8 trillium un
459	38	43.7	518	2	Q9TN83	Q9tn83 asparagus f
460	38	43.7	531	2	Q920A8	Q920a8 mus musculu
461	38	43.7	532	2	Q6P9J3	Q6p9j3 mus musculu
462	38	43.7	534	2	Q96PK1	Q96pk1 homo sapien
463	38	43.7	534	2	Q6PIU2	Q6piu2 xenopus tro
464	38	43.7	536	2	Q9BSA4	Q9bsa4 homo sapien
465	38	43.7	551	2	Q89E23	Q89ez3 bradyrhizob
466	38	43.7	572	2	Q7NVS7	Q7nvs7 chromobacte
467	38	43.7	584	2	Q74IP6	Q74ip6 lactobacill
468	38	43.7	588	2	Q8VPI8	Q8vpi8 lactobacill
469	38	43.7	591	2	Q9K1Q4	Q9k1q4 vibrio chol
470	38	43.7	601	2	Q6FK29	Q6fk29 candida gla
471	38	43.7	612	2	Q9HU20	Q9hu20 pseudomonas
472	38	43.7	616	2	Q64P12	Q64p12 bacteroides
473	38	43.7	619	2	Q9A2R4	Q9a2r4 caulobacter
474	38	43.7	645	2	Q67UO9	Q67u9 oryza sativ
475	38	43.7	650	2	Q42722	Q42722 daucus caro
476	38	43.7	657	2	Q9GDW0	Q9gdw0 streptopus
477	38	43.7	657	2	Q9GDW1	Q9gdw1 streptopus
478	38	43.7	657	2	Q9GDW5	Q9gdw5 scolioses m
479	38	43.7	660	2	Q9GDW3	Q9gdw3 scolioses b
480	38	43.7	671	2	Q75HR4	Q75hr4 oryza sativ
481	38	43.7	672	2	Q95AT4	Q95at4 areca vesti
482	38	43.7	694	2	Q95AQ6	Q95aq6 beccariopho
483	38	43.7	698	2	Q95AS3	Q95as3 wettinia hi
484	38	43.7	703	2	Q6LFD2	Q6lfd2 plasmodium
485	38	43.7	710	2	Q87DS8	Q87ds8 xylella fae
486	38	43.7	710	2	Q9PDL6	Q9pdl6 xylella fae
487	38	43.7	727	1	DOC7_MOUSE	Q8ria4 mus musculu
488	38	43.7	732	2	Q61565	Q61565 crassostrea
489	38	43.7	745	2	Q63TM1	Q63tm1 burkholderi
490	38	43.7	760	2	Q8J1E2	Q8j1e2 piromyces e
491	38	43.7	772	2	Q8XYD2	Q8xyd2 ralstonia s
492	38	43.7	788	2	Q9VGL9	Q9vgl9 drosophila
493	38	43.7	835	2	Q6FUJ7	Q6fuj7 candida gla
494	38	43.7	839	2	Q6PUJ7	Q6puj7 mus musculu
495	38	43.7	846	2	Q6BSQ7	Q6bsq7 debaryomyce
496	38	43.7	864	2	Q68395	Q68395 thauera aro
497	38	43.7	864	2	Q8L1A3	Q8l1a3 thauera sp.
498	38	43.7	921	2	Q7SFM0	Q7sfm0 neurospora
499	38	43.7	928	2	Q8ZC53	Q8zcs53 oryza sativ
500	38	43.7	1132	2	Q7NAF6	Q7naf6 mycoplasma

ALIGNMENTS

RESULT 1

Q9TSJ6 PRELIMINARY; PRT; 39 AA.

Q9TSJ6

AC Q9TSJ6; PRT; 39 AA.

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Acetylcholinesterase T-subunit (Fragment).

GN Name=ACHe;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=983159754; PubMed=9693127;

RA Mendelson I., Kronman C., Ariel N., Shaffer A., Velan B.;

RT "Bovine acetylcholinesterase: cloning, expression and

RT characterization.";

RL Biochem. J. 334:251-259(1998).

DR EMBL; AF061816; AAC64269.1; -.

FT NON_TER 1 1

FT NON_TER 39 39

SQ SEQUENCE 39 AA; 4959 MW; 72F3379D0F8B6557 CRC64;

Query Match 100.0%; Score 87; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 7.9e-06; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0;

QY 1 AEFHRWSSYVHWK 14

Db 11 AEFHRWSSYVHWK 24

RESULT 2

```

Q86YX9
ID Q86YX9 PRELIMINARY; PRT; 526 AA.
AC Q86YX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apoptosis-related acetylcholinesterase (EC 3.1.1.7).
GN Name=ARACHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang L., Zhang X.J.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF342470; AAC02948.1; -.
DR HSP; P22303; IFSU.
DR GO; GO:0003990; F:acetylcholinesterase activity; IEA.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hydrolase. 526 AA; 58352 MW; F885F41EDFF39DB CRC64;
SQ SEQUENCE 526 AA; 58352 MW; F885F41EDFF39DB CRC64;

Query Match 100.0%; Score 87; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. NO. 9.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSVMVHWK 14
Db 498 AEFHRSSVMVHWK 511

RESULT 3
ID ACES_RABIT STANDARD; PRT; 584 AA.
AC Q29499;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE) (Fragment).
GN Name=ACE;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Ubblo O., L'Hermite Y., Tallea V., Toutant J.-P., Chatonnet A.;
RL rabbit tissues and during development."
RT "Acetylcholinesterase and butyrylcholinesterase expression in adult
RL Eur. J. Biochem. 225:115-124(1994).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Homotrimer; composed of disulfide-linked homodimers.
CC Interacts with PRIMA1. The interaction with PRIMA1 is required to
CC anchor it to the basal lamina of cells and organize into tetramers
CC (By similarity).
CC -1- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
CC cholinesterase, with a collagen-like part disulfide-bonded to the
CC catalytic part. A different, globular type of cholinesterase
CC occurs on the outer surfaces of cell membranes, including those of
CC erythrocytes.

Q86YX9
ID Q86YX9 PRELIMINARY; PRT; 526 AA.
AC Q86YX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apoptosis-related acetylcholinesterase (EC 3.1.1.7).
GN Name=ARACHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang L., Zhang X.J.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF342470; AAC02948.1; -.
DR HSP; P22303; IFSU.
DR GO; GO:0003990; F:acetylcholinesterase activity; IEA.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hydrolase. 526 AA; 58352 MW; F885F41EDFF39DB CRC64;
SQ SEQUENCE 526 AA; 58352 MW; F885F41EDFF39DB CRC64;

Query Match 100.0%; Score 87; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. NO. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSVMVHWK 14
Db 556 AEFHRSSVMVHWK 569

RESULT 4
ID ACES_FELCA STANDARD; PRT; 611 AA.
AC Q62763; O62762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN Name=ACHE;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RL Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma."
RL Biochem. Pharmacol. 60:479-487(2000).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers.

-1- MISCELLANEOUS: This is the catalytic subunit of an asymmetric or
soluble form of AChE.
-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
EMBL; U05036; AAA53235.1; -.
HSP; P22303; IFSU.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000997; Cholinesterase.
Pfam; PF00135; Coesterase; 1.
PRINTS; PR00878; CHOLNESTRASE.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
Serine esterase; Signal; Synapse.
NON_TER 1 1 Potential.
SIGNAL <1 1 Acetylcholinesterase.
CHAIN 2 584 Acyl-ester intermediate. (By similarity).
ACT_SITE 204 204 Charge relay system (By similarity).
ACT_SITE 335 335 Charge relay system (By similarity).
ACT_SITE 448 448 Charge relay system (By similarity).
DISULFID 70 97 By similarity.
DISULFID 258 273 By similarity.
DISULFID 410 530 By similarity.
DISULFID 581 581 Interchain (By similarity).
CARBOHYD 266 266 N-linked (GLCNAC...) (Potential).
CARBOHYD 351 351 N-linked (GLCNAC...) (Potential).
CARBOHYD 465 465 N-linked (GLCNAC...) (Potential).
SEQUENCE 584 AA; 64630 MW; 2AE157F3063649FE CRC64;

Query Match 100.0%; Score 87; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. NO. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSVMVHWK 14
Db 556 AEFHRSSVMVHWK 569

RESULT 4
ID ACES_FELCA STANDARD; PRT; 611 AA.
AC Q62763; O62762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN Name=ACHE;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RL Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma."
RL Biochem. Pharmacol. 60:479-487(2000).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers.

```

```

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Kidney;
RC TISSUE=Kidney;
RA Mendelson I., Kronman C., Ariel N., Shafferman A., Velan B.;
RA MEDLINE=98359754; PubMed=9693127;
RT "Bovine acetylcholinesterase: cloning, expression and
RL characterization.";
RL Biochem. J. 334:251-259(1998).
RN [2]
RN SEQUENCE OF 31-613 (ISOFORM H).
RC TISSUE=Fetal serum;
RC MEDLINE=90306335; PubMed=2365060; DOI=10.1016/0014-5793(90)81522-P;
RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
RA "Complete amino acid sequence of fetal bovine serum
RT acetylcholinesterase and its comparison in various regions with other
RT cholinesterases.";
RL FEBS Lett. 266:123-127(1990).
CC -I- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -I- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -I- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers (By similarity). Isoform H generates GPI-anchored
CC dimers; disulfide linked. Isoform T generates multiple structures,
CC ranging from monomers and dimers to collagen-tailed and
CC asphobic-tailed forms, in which catalytic tetramers are
CC associated with anchoring proteins that attach them to the basal
CC lamina or to cell membranes. In the collagen-tailed forms, isoform
CC T subunits are associated with a specific collagen, COLQ, which
CC triggers the formation of isoform T tetramers, from monomers and
CC dimers.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=P23795-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P23795-2; Sequence=VSP_001455;
CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF061815; AAC64270.1; -.
DR EMBL; AF061813; AAC64270.1; JOINED.
DR EMBL; AF061814; AAC64270.1; JOINED.
DR HSP; P23303; 1F8U.
DR GlycoSuiteDB; P23795; -.
DR InterPro; IPR02018; CarboxylesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNSTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydrolase; Membrane; Neurotransmitter degradation; Serine esterase;
KW Signal; Synapse.
KW SIGNAL 1 30
FT CHAIN 31 613 Acetylcholinesterase.
FT ACT_SITE 233 233 Acyl-ester intermediate (By similarity).
FT ACT_SITE 364 364 Charge relay system (By similarity).
FT ACT_SITE 477 477 Charge relay system (By similarity).
FT DISULFID 999 126 By similarity.

```



```

FT DISULFID 287 302 By similarity.
FT DISULFID 439 559 By similarity.
FT DISULFID 610 610 Interchain (By similarity).
FT CARBOHYD 91 91 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 295 295 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 380 380 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 494 494 N-linked (GlcNAc...) (Probable).
FT VARSPLIC 574 613 DTIDEAERQWKAFFHRSSVYVWVKQFDHYSKQDRCSOL
FT FT -> ASEAPCTCGPAGHEAARPRPGPLPLLLLLFLLSRL
FT FT LRL (in isoform H).
FT FT /FTID=VSP 001455.
FT FT R -> E (in Ref. 2).
FT FT T -> V (in Ref. 2).
FT FT W -> S (in Ref. 2).
FT FT S -> H (in Ref. 2).
FT FT H -> V (in Ref. 2).
FT FT L -> W (in Ref. 2).
FT FT D -> A (in Ref. 2).
FT FT EVRRGL -> GVFOAS (in Ref. 2).
FT FT S -> N (in Ref. 2).
FT FT S -> N (in Ref. 2).
SQ SEQUENCE 613 AA; 67663 MW; 698D4F0DF8624B12 CRC64;

Query Match 100.0%; Score 87; DB 1; Length 613;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVYVWVK 14
Db 585 AEFHRSSVYVWVK 598
|||||
|||||

RESULT 6
ACES HUMAN STANDARD; PRT; 614 AA.
AC P22303; Q16169; Q9EXF7.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088577; PubMed=2263619;
RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnat A., Neville L.,
RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA Zakut H.;
RT "Molecular cloning and construction of the coding region for human
RT acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN [2]
RP SEQUENCE OF 521-614 FROM N.A.
RX MEDLINE=21138439; PubMed=8299725; DOI=10.1093/nar/29.6.1352;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [3]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=94131004; PubMed=8299725; DOI=10.1006/exr.1994.1039;
RA Karpel R., Ben-Aziz-Aloya R., Sternfeld M., Ehrlich G., Ginzberg D.,
RA Tarroni P., Clemenit F., Zakut H., Soreq H.;
RT "Expression of three alternative acetylcholinesterase messenger RNAs
RT in human tumor cell lines of different tissue origins.";
RL Exp. Cell Res. 210:268-277(1994).
RN [4]
RP PARTIAL SEQUENCE.
RC TISSUE=Erythrocyte;

```

```

RX MEDLINE=89232136; PubMed=2714437; DOI=10.1016/0014-5793(89)81352-3;
RA Chhajlani V., Derr D., Barles B., Schnell E., August T.;
RT "Purification and partial amino acid sequence analysis of human
RT erythrocyte acetylcholinesterase.";
RL FEBS Lett. 247:279-282(1989).
RN [5]
RP MUTAGENESIS OF CYS-611.
RX MEDLINE=92084699; PubMed=1748670;
RA Velan B., Grosfeld H., Kronman C., Leitner M., Gozes Y., Lazar A.,
RA Flashner Y., Marcus D., Cohen S., Shaffer A.;
RT "The effect of elimination of interaunit disulfide bonds on the
RT activity, assembly, and secretion of recombinant human
RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT mutant.";
RL J. Biol. Chem. 266:23977-23984(1991).
RN [6]
RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX MEDLINE=92388112; PubMed=1517212;
RA Shaffer A., Kronman C., Flashner Y., Leitner M., Grosfeld H.,
RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT "Mutagenesis of human acetylcholinesterase. Identification of residues
RT involved in catalytic activity and in polypeptide folding.";
RL J. Biol. Chem. 267:17640-17648(1992).
RN [7]
RP 3D-STRUCTURE MODELING OF 35-574.
RX MEDLINE=98304745; PubMed=9640563;
RA Felder C.E., Botti S.A., Lifson S., Silman I., Sussman J.L.;
RT "External and internal electrostatic potentials of cholinesterase
RT models.";
RL J. Mol. Graph. Model. 15:318-327(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.
RX MEDLINE=20508217; PubMed=11053835; DOI=10.1107/S0907444900010659;
RA Kvyter G., Harel M., Giles K., Tokar L., Velan B., Lazar A.,
RA Kronman C., Barak D., Ariel N., Shaffer A., Silman I.,
RA Sussman J.L.;
RT "Structures of recombinant native and E202Q mutant human
RT acetylcholinesterase complexed with the snake-venom toxin fasciculin-
RT II.";
RL Acta Crystallogr. D 56:1385-1394(2000).
RN [9]
RP VARIANT BLOOD GROUP YT(B) ASN-353.
RX MEDLINE=93256075; PubMed=8488842;
RA Bartels C.F., Zelinski T., Lockridge O.;
RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
RT accounts for Yt blood group polymorphism.";
RL Am. J. Hum. Genet. 52:928-936(1993).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Homotrimer; composed of disulfide-linked homodimers.
CC Interacts with PRIMA1. The interaction with PRIMA1 is required to
CC anchor it to the basal lamina of cells and organize into tetramers
CC (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P22303-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P22303-2; Sequence=VSP 001457;
CC -1- POLYMORPHISM: ACHE is responsible for the Yt blood group system.
CC The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group
CC antigens is a single variation in position 353; His-353
CC corresponds to Yt(a) and the rare variant with Asn-353 to Yt(b).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -1- DATABASES: NMR-Blood group antigen mutation database;
CC NOTE=Yt blood group system;
CC WWW="http://www.bioc.aecom.edu/bgmmt/yt.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```


RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN INTERACTION WITH PRIMA1.
RP MEDLINE=21664287; PubMed=11804574; DOI=10.1016/S0896-6273(01)00584-0;
RX Bourne Y., Taylor P., Marchot P.;
RA "PRIMA: the membrane anchor of acetylcholinesterase in the brain.";
RT "PRIMA: the membrane anchor of acetylcholinesterase in the brain.";
RL Neuron 33:275-285(2002).
[5]
RN X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX MEDLINE=96067648; PubMed=8521480; DOI=10.1016/0092-8674(95)90128-0;
RA Bourne Y., Taylor P., Marchot P.;
RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
RT the complex.";
RL Cell 83:503-512(1995).
[6]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=99115643; PubMed=9915834; DOI=10.1074/jbc.274.5.2963;
RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
RT occluding loop in a tetrameric assembly.";
RL J. Biol. Chem. 274:2963-2970(1999).
[7]
RN X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 34-573 IN COMPLEX WITH
RP INHIBITOR.
RX PubMed=12505979; DOI=10.1093/emboj/cdg005;
RA Bourne Y., Taylor P., Radic Z., Marchot P.;
RT "Structural insights into ligand interactions at the
RT acetylcholinesterase peripheral anionic site.";
RL EMBO J. 22:1-12(2003).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Isoform H generates GPI-anchored dimers, disulfide
CC linked. Isoform T generates multiple structures, ranging from
CC monomers and dimers to collagen-tailed and hydrophobic-tailed
CC forms, in which catalytic tetramers are associated with anchoring
CC proteins that attach them to the basal lamina or to cell
CC membranes. In the collagen-tailed forms, isoform T subunits are
CC associated with a specific collagen, COLQ, which triggers the
CC formation of isoform T tetramers, from monomers and dimers (By
CC similarity). Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=P21836-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P21836-2; Sequence=Not described;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Predominates in most expressing tissues except
CC erythrocytes where a glycopospholipid-attached form of AChE
CC predominates.
CC -1- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
CC cholinesterase, with a collagen-like part disulfide-bonded to the
CC catalytic part. A different, globular type of cholinesterase
CC occurs on the outer surfaces of cell membranes, including those of
CC erythrocytes.
CC -1- MISCELLANEOUS: This is the catalytic subunit of an asymmetric or
CC soluble form of AChE.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X56518; CAA39867.1; --
DR EMBL; AF312033; AAK28816.1; --
DR EMBL; BC046327; AAH46327.1; --
DR PIR; JH0314; JH0314.
DR PDB; 1C2B; X-ray; A=35-573.
DR PDB; 1C2O; X-ray; A/B/C/D=36-574.
DR PDB; 1J06; X-ray; A/B=32-574.
DR PDB; 1J07; X-ray; A/B=32-574.
DR PDB; 1K06; X-ray; A=32-580.
DR PDB; 1MAA; X-ray; A/B/C/D=32-578.
DR PDB; 1MAH; X-ray; A=32-574.
DR PDB; 1NSH; X-ray; A/B=32-572.
DR PDB; 1NSR; X-ray; A/B=32-574.
DR PDB; 1Q83; X-ray; A/B=1-580.
DR MGD; MGI:87876; Ache.
DR GO; GO:0045202; C:synapse; IDA.
DR InterPro; IPR00122; CarboxylesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW 3D-structure; Alternative splicing; Glycoprotein; Hydrolase; Membrane;
KW Neurotransmitter degradation; Serine esterase; Signal; Synapse.
FT SIGNAL 1 31
FT CHAIN 32 614 Acetylcholinesterase.
FT ACT_SITE 234 234 Acyl-ester intermediate.
FT ACT_SITE 365 365 Charge relay system.
FT ACT_SITE 478 478 Charge relay system.
FT DISULFID 100 127
FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611 Interchain (By similarity).
FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 381 381 N-linked (GlcNAc...)
FT CARBOHYD 495 495 N-linked (GlcNAc...)
FT HELIX 37 39
FT STRAND 40 43
FT TURN 44 45
FT STRAND 46 49
FT STRAND 51 55
FT TURN 56 57
FT STRAND 58 67
FT STRAND 69 69
FT HELIX 74 76
FT TURN 77 78
FT STRAND 83 83
FT STRAND 90 92
FT STRAND 94 94
FT STRAND 99 100
FT TURN 109 110
FT HELIX 112 115
FT TURN 116 117
FT STRAND 123 124
FT STRAND 129 135
FT STRAND 143 149
FT TURN 153 155
FT TURN 159 160
FT HELIX 162 164
FT HELIX 167 173
FT STRAND 176 180
FT HELIX 185 189
FT TURN 193 194
FT HELIX 202 217
FT HELIX 218 221
FT TURN 222 222
FT STRAND 223 233
FT TURN 234 234
FT HELIX 235 244
FT TURN 245 245
FT HELIX 247 250
FT TURN 251 252

```

FT STRAND 255 259
FT STRAND 270 271
FT HELIX 272 285
FT TURN 286 287
FT HELIX 297 304
FT TURN 305 306
FT HELIX 309 315

Query Match 100.0%; Score 87; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
    |||||
Db 586 AEFHRWSSVMVHWK 599

RESULT 8
ACES RAT STANDARD; PRT; 614 AA.
AC P37136;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=Ache;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM T).
RX MEDLINE=93107932; PubMed=8417155;
RA Legay C., Bon S., Vernier P., Cousen F., Massoulie J.;
RT "Cloning and expression of a rat acetylcholinesterase subunit:
RT generation of multiple molecular forms and complementarity with a
RT Torpedo collagenic subunit.";
RL J. Neurochem. 60:337-346(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX MEDLINE=93114454; PubMed=8417973; DOI=10.1016/0014-5793(93)81155-S;
RA Legay C., Bon S., Massoulie J.;
RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT acetylcholinesterase.";
RL FEBS Lett. 315:163-166(1993).
CC -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
CC Catalytic forms H (GPI-anchor dimer) and T (asymmetric collagen-
CC tailed), which differ in their C-terminus, account for all types
CC of known ACHE forms. Interacts with PRIMA1. The interaction with
CC PRIMA1 is required to anchor it to the basal lamina of cells and
CC organize into tetramers (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=T;
CC IsoId=P37136-1; Sequences=Displayed;
CC Name=H;
CC IsoId=P37136-2; Sequences=VSP_001458;
CC Name=R;
CC IsoId=P37136-3; Sequences=VSP_001459;
CC Note=May be not functional;
CC -!- TISSUE SPECIFICITY: Has been found in central nervous system and
CC muscle. Found in embryonic liver and spleen but not in adult
CC liver.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

```

or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S50879; AAB24586.1; -.
CC EMBL; X70140; CAA49717.1; -.
CC EMBL; X70141; CAA49718.1; -.
CC PIR; JH0811; JH0811.
CC HSSP; P21836; IMAA.
CC RGD; 69313; Ache.
CC InterPro; IPR002018; CarbesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLNESTRASE.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00942; CARBOXYLESTERASE_B_2; 1.
KW Alternative splicing; Glycoprotein; Hydrolase; Membrane;
KW Neurotransmitter degradation; Serine esterase; Signal; Synapse.
FT SIGNAL 1 31 Potential.
FT CHAIN 32 614 Acetylcholinesterase.
FT ACT_SITE 234 234 Acyl-ester intermediate (By similarity).
FT ACT_SITE 365 365 Charge relay system (By similarity).
FT ACT_SITE 478 478 Charge relay system (By similarity).
FT DISULFID 100 127 By similarity.
FT DISULFID 288 303 By similarity.
FT DISULFID 440 560 By similarity.
FT DISULFID 611 611 Interchain (By similarity).
FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 381 381 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 575 614 DTLDEAEKQWKAEFHRWSSVMVHWKQFDHYSKQERCSDL
FT -> ATEVPTCTCPAHEAAAPPGPALSLSLFLFLHSG
FT LRWL (in isoform H).
FT /FTId=VSP_001458.
FT DTLDEAEKQWKAEFHRWSSVMVHWKQFDHYSKQERCSDL
FT isoform R).
FT -> GRGVGKQGMKAARVGTGRKGKGRM (in
FT /FTId=VSP_001459.
SQ SEQUENCE 614 AA; 68196 MW; 2EDAETD46282E7C0 CRC64;

Query Match 100.0%; Score 87; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
    |||||
Db 586 AEFHRWSSVMVHWK 599

RESULT 9
Q67BC1
ID Q67BC1 PRELIMINARY; PRT; 614 AA.
AC Q67BC1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Acetylcholinesterase T-form.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Cohen O., Kronman C., Velan B., Shafferman A.;
RT "Macaca mulatta acetylcholinesterase gene.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC EMBL; AY372522; AAR24295.1; JOINED.
CC EMBL; AY372523; AAR24295.1; JOINED.
CC EMBL; AY372526; AAR24295.1; JOINED.
CC EMBL; AY372524; AAR24295.1; JOINED.
CC InterPro; IPR002018; CarbesteraseB.
CC InterPro; IPR000997; Cholinesterase.

```

DR	InterPro; IPR000379; Ser_estrs.
DR	Pfam; PF00135; Coesterase; 1.
DR	PRINTS; PR00878; CHOLNESTRASE.
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
SQ	SEQUENCE 614 AA; 67772 MW; 7A4FCE096015C5C CRC64;
 Query Match 100.0%; Score 87; DB 2; Length 614; Best Local Similarity 100.0%; Pred.No.0.00011; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 AEFHRSSVYVHWK 14 586 AEFHRSSVYVHWK 599
Dd	
 RESULT 10 ACES_ELEEL STANDARD; PRT; 633 AA. AC O42275; DT 16-OCT-2001 (Rel. 40, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 25-OCT-2004 (Rel. 45, Last annotation update) DT Acetylcholinesterase precursor (EC 3.1.1.7) (AChE). OS Electrophorus electricus (Electric eel). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes; OC Eleutherozoa; Euteleostomi; Osteichthyes; Characiformes; OX Eucarcharia; Eucarcharia; Eucarcharia; Eucarcharia; OX NCBI_TaxID=8005; RN [1] RS SEQUENCE FROM N.A. RP MEDLINE=98070504; PubMed=9407087; DOI=10.1074/jbc.272.52.33045; RX Simon S., Massoulie J.; RT "Cloning and expression of acetylcholinesterase from Electrophorus." RT Splicing pattern of the 3' exons in vivo and in transfected mammalian cells."; RL J. Biol. Chem. 272:33045-33055(1997). CC -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse. CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate. CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family. ----- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch). ----- CC EMBL; AF030422; AAB86606.1; -. CC HSP; P04058; IH23 DR InterPro; IPR002018; CarbestraseB. DR InterPro; IPR000997; Cholinesterase. DR InterPro; IPR000379; Ser_estrs. PFam; PF00135; Coesterase; 1. DR PRINTS; PR00878; CHOLNESTRASE. DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1. DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1. KW Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation; FT Signal peptide; Signal; Synapse. FT SIGNAL 1 23 Potential. FT CHAIN 24 633 Acetylcholinesterase. FT ACT_SITE 225 225 Acyl-ester intermediate (By similarity). FT ACT_SITE 352 352 Charge relay system (By similarity). FT ACT_SITE 494 494 Charge relay system (By similarity). FT DISULFID 91 118 By similarity. FT FT 279 290 By similarity. FT FT 427 579 By similarity. FT DISULFID 630 630 Interchain (By similarity). FT FT 133 133 N-linked (GlcNAc...) (potential). FT CARBOHYD 184 184 N-linked (GlcNAc...) (potential). FT CARBOHYD 263 283 N-linked (GlcNAc...) (potential). FT CARBOHYD 368 368 N-linked (GlcNAc...) (potential).	

```

CC -|- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -|- SUBUNIT: Dimers and collagen-tailed forms, in which catalytic
CC tetramers are associated with anchoring proteins that attach them
CC to the basal lamina or to cell membranes. In the collagen-tailed
CC forms, subunits are associated with a specific collagen, COLQ,
CC which triggers the formation of isoform T tetramers from dimers.
CC -|- MISCELLANEOUS: No other isoforms exist. This protein corresponds
CC to the T isoform in other species.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ251640; CAC19790.1; -.
CC HSSP; P04058; 1H23.
CC ZFIN; ZDB-GENE-010906-1; ache.
CC InterPro; IPR002018; CarbesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLINESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW Serine esterase; Signal; Synapse.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 634 Acetylcholinesterase.
FT ACT_SITE 225 225 Acyl-ester intermediate (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT ACT_SITE 495 495 Charge relay system (By similarity).
FT DISULFID 91 118 By similarity.
FT DISULFID 279 290 By similarity.
FT DISULFID 427 580 By similarity.
FT DISULFID 631 631 Interchain (By similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 512 512 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 592 592 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 634 AA; 71998 MW; 47F348EA8A7C1E52 CRC64;

Query Match 92.0%; Score 80; DB 1; Length 634;
Best Local Similarity 92.3%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFHRWSYVHWK 14
Db 607 EFHRWSYVHWK 619

RESULT 13
ACES_BUNFA STANDARD; PRT; 606 AA.
AC Q92035; O73748; Q10720;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
OS Bungarus fasciatus (Banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8613;
RN [1]_TaxID=8613;
RP SEQUENCE FROM N.A. (ISOFORM S).
RC TISSUE=venom gland;
RX MEDLINE=96279007; PubMed=8662867; DOI=10.1074/jbc.271.25.15099;

```

```

RA Cousin X., Bon S., Duval N., Massoulie J., Bon C.;
RT "Cloning and expression of acetylcholinesterase from Bungarus
RT fasciatus venom. A new type of COOH-terminal domain; involvement of a
RT positively charged residue in the peripheral site.";
RL J. Biol. Chem. 271:15099-15108(1996).
RN [2]
RP SEQUENCE OF 512-606 FROM N.A. (ISOFORMS S AND T), SUBUNIT, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Liver, and Muscle;
RC MEDLINE=98212017; PubMed=9545320; DOI=10.1074/jbc.273.16.9812;
RX Cousin X., Bon S., Massoulie J., Bon C.;
RT "Identification of a novel type of alternatively spliced exon from the
RT acetylcholinesterase gene of Bungarus fasciatus. Molecular forms of
RT acetylcholinesterase in the snake liver and muscle.";
RL J. Biol. Chem. 273:9812-9820(1998).
RN [3]
RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.
RC TISSUE=Venom;
RC MEDLINE=96244524; PubMed=8674549; DOI=10.1016/0014-5793(96)00447-4;
RA Cousin X., Creminon C., Grassi J., Meflah K., Cornu G., Sallou B.,
RA Bon S., Massoulie J., Bon C.;
RT "Acetylcholinesterase from Bungarus venom: a monomeric species.";
RL FEBS Lett. 387:196-200(1996).
CC -|- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -|- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -|- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,
CC including collagen-tailed forms.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=Q92035-2; Sequence=Displayed;
CC Name=S;
CC IsoId=Q92035-1; Sequence=VSP_008215;
CC -|- TISSUE SPECIFICITY: Liver and muscle contain both isoform T and
CC isoform S. Venom gland predominantly contains isoform S.
CC -|- PTM: The N-terminus is blocked.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -|- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U54591; AAC59905.1; -.
CC EMBL; AF045238; AAC16420.1; -.
CC EMBL; AF045238; AAC16421.1; -.
CC HSSP; P04058; 1H23.
CC InterPro; IPR002018; CarbesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000908; Fish_Ache.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLINESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydrolase; Membrane; Neurotransmitter degradation; Serine esterase;
KW Signal; Synapse.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 606 Acetylcholinesterase.
FT ACT_SITE 231 231 Acyl-ester intermediate (By similarity).
FT ACT_SITE 358 358 Charge relay system (By similarity).
FT ACT_SITE 471 471 Charge relay system (By similarity).
FT DISULFID 98 125 By similarity.
FT DISULFID 285 296 By similarity.
FT DISULFID 433 552 By similarity.
FT DISULFID 603 603 Interchain (in isoform T) (By
FT similarity).

```

```

FT CARBOHYD 289 289 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 484 484 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 564 564 N-linked (GlcNAc... ) (Potential).
FT VARSPLIT 567 606 DNEIEAEQWKLFEHLMSAYMMHWKSFQDHYNKQDRCSSEL
FT VARSPLIT 567 606 -> VDPPEADRRRSARA (in isoform S).
FT MUTAGEN 101 101 /FTid=VSP_008215.
FT MUTAGEN 101 101 M->Y: Increases peripheral site ligand
FT MUTAGEN 316 316 binding.
FT MUTAGEN 316 316 K->D: Increases peripheral site ligand
FT CONFLICT 268 268 T -> S (in Ref. 3).
FT CONFLICT 350 350 V -> L (in Ref. 3).
SQ SEQUENCE 606 AA; 68074 MW; B95998AERA0E5709 CRC64;

Query Match 80.5%; Score 70; DB 1; Length 606;
Best Local Similarity 76.9%; Pred. No. 0.035;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EFHRWSSYVHWK 14
Db 579 EFHLWSAYMMHWK 591

RESULT 14
Q9JUK1 PRELIMINARY; PRT; 597 AA.
AC Q9JUK1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUP=Heart;
RA Li B., Stribley J., Ticu A., Xie W., Schopfer L.M., Hammond P.,
RA BrimiJoin S., Hinrichs S.H., Lockridge O.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUP=Heart;
RA Ticu A.M., Lockridge O., Bartels C.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF244349; AAF44713.1; -.
DR HSSP; P06276; 1P01.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR HYDROLASE.
SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7EEAC CRC64;

Query Match 74.7%; Score 65; DB 2; Length 597;
Best Local Similarity 71.4%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFRWSSYVHWK 14
Db 568 AGFRWSSYVMDWK 581

RESULT 15
ACES_CHICK

```

```

ID ACES_CHICK STANDARD; PRT; 767 AA.
AC P36196;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUP=Muscle;
RA Randall W.R., Rimer M., Gough N.R.;
RL "Cloning and analysis of chicken acetylcholinesterase transcripts from
muscle and brain.";
RL Biochim. Biophys. Acta 1218:453-456(1994).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Oligomer composed of disulfide-linked homodimers.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.18b-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC EMBL; U03472; AAA60456.1; -.
DR PIR; S47639; S47639.
DR HSSP; P21836; INSM.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW Serine esterase; Signal; Synapse.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 767 Acetylcholinesterase.
FT ACT_SITE 227 227 Acyl-ester intermediate (By similarity).
FT ACT_SITE 520 520 Charge relay system (By similarity).
FT ACT_SITE 633 633 Charge relay system (By similarity).
FT DISULFID 94 121 By similarity.
FT DISULFID 281 292 By similarity.
FT DISULFID 595 713 By similarity.
FT DISULFID 764 764 Interchain (By similarity).
FT CARBOHYD 285 285 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 650 650 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 725 725 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 767 AA; 83020 MW; B1B3DF29C31F6062 CRC64;

Query Match 74.7%; Score 65; DB 1; Length 767;
Best Local Similarity 76.9%; Pred. No. 0.24;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EFHRWSSYVHWK 14
Db 740 EFHRWSSYVGRWR 752

RESULT 16
Q96HL2 PRELIMINARY; PRT; 64 AA.
ID Q96HL2
AC Q96HL2;

```

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCHE protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008396; AA08396.1; -.
DR HSSP; P06276; 1P01.
SQ SEQUENCE 64 AA; 7861 MW; 67A0BB30F441F05F CRC64;

Query Match 71.3%; Score 62; DB 2; Length 64;
Best Local Similarity 64.3%; Pred. No. 0.064;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
DB 35 AGFHRWNNYMDWK 48
| | | | | : | | | | |
RESULT 17
CHLE HORSE
ID CHLE HORSE STANDARD; PRT; 574 AA.
AC P81908;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EQ-
BCHE).
GN Name=BCHE;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;
RT "Amino acid sequence of horse serum butyrylcholinesterase.";
RL (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.
(eds.);
RL Structure and function of cholinesterases and related proteins,

RL pp.145-146, Plenum Press, New York and London (1998).
CC -|- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -|- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -|- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -|- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR HSSP; P21836; 1NSM.
DR InterPro; IPR002018; Carboxylesterase8.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrb.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine esterase.
FT ACT SITE 198 198 Acyl-ester intermediate (By similarity).
FT ACT SITE 325 325 Charge relay system (By similarity).
FT ACT SITE 438 438 Charge relay system (By similarity).
FT DISULFID 65 92 By similarity.
FT DISULFID 252 263 By similarity.
FT DISULFID 400 519 By similarity.
FT DISULFID 571 571 Interchain (By similarity).
FT CARBOHYD 57 57 N-linked (GLCNAC. . .).
FT CARBOHYD 106 106 N-linked (GLCNAC. . .).
FT CARBOHYD 241 241 N-linked (GLCNAC. . .).
FT CARBOHYD 256 256 N-linked (GLCNAC. . .).
FT CARBOHYD 341 341 N-linked (GLCNAC. . .).
FT CARBOHYD 455 455 N-linked (GLCNAC. . .).
FT CARBOHYD 481 481 N-linked (GLCNAC. . .).
FT CARBOHYD 486 486 N-linked (GLCNAC. . .).
SQ SEQUENCE 574 AA; 65641 MW; 07755EE9PB9CB33E CRC64;

Query Match 71.3%; Score 62; DB 1; Length 574;
Best Local Similarity 64.3%; Pred. No. 0.51;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
DB 545 AGFHRWNNYMDWK 558
| | | | | : | | | | |
RESULT 18
CHLE HUMAN
ID CHLE HUMAN STANDARD; PRT; 602 AA.
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCHE; Synonyms=CHE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90212557; PubMed=2322535;
RA Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.;
RT "Structure of the gene for human butyrylcholinesterase. Evidence for a
RT single copy.";
RL Biochemistry 29:124-131(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal;
RX MEDLINE=87231856; PubMed=3035536;
RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;
RT "Isolation and characterization of full-length cDNA clones coding for

RT cholinesterase from fetal human tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86016155; PubMed=3477799;
RA McTiernan C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.,
RA "Brain cDNA clone for human cholinesterase.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.;
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.;
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase.";
RL J. Biol. Chem. 262:12945-12952(1987).
RN [7]
RP REVIEW.
RX MEDLINE=89149758; PubMed=3067729;
RA Lockridge O.;
RT "Structure of human serum cholinesterase.";
RL Bioessays 9:125-128(1988).
RN [8]
RP VARIANT ATYPICAL GLY-98.
RX MEDLINE=89128896; PubMed=2915989;
RA McGuire M.C., Nequeira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA van der Spek A.F.L., Lockridge O., la Du B.N.;
RT "Identification of the structural mutation responsible for the
RT dibucaine-resistant (atypical) variant form of human serum
RT cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [9]
RP VARIANT ILE-358.
RX MEDLINE=96287386; PubMed=8680411;
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Moriwaki K.;
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholesterolemia";
RL Hum. Mutat. 6:349-351(1995).
CC -I- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a

CC carboxylic acid anion.
CC -I- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -I- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -I- DISEASE: Mutant alleles of CHE1 are responsible for
CC hypocholesterolemia resulting in exanthematous sensitivity.
CC Homozygous persons sustain prolonged apnea after administration of
CC the muscle relaxant suxamethonium in connection with surgical
CC anesthesia.
CC -I- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M32391; AAA99296.1; -
CC EMBL; M32389; AAA99296.1; JOINED.
CC EMBL; M32390; AAA99296.1; JOINED.
CC EMBL; M16541; AAA98113.1; -
CC EMBL; M16474; AAA52015.1; -
CC EMBL; BC018141; AAH18141.1; -
CC PIR; A33769; ACHU.
CC PDB; 1EHO; Model; A=30-560.
CC PDB; 1EHQ; Model; A=30-560.
CC PDB; 1P01; X-ray; A=29-557.
CC PDB; 1P0M; X-ray; A=29-557.
CC PDB; 1P0P; X-ray; A=29-557.
CC PDB; 1P0Q; X-ray; A=29-557.
CC Genex; HGNC:983; BCHE.
CC H-invDB; HIX003828; -
CC MIM; 177400; -
CC GO; GO:0001540; F:beta-amyloid binding; NAS.
CC GO; GO:0003824; F:catalytic activity; NAS.
CC GO; GO:0004104; F:cholinesterase activity; NAS.
CC GO; GO:0019899; F:enzyme binding; NAS.
CC GO; GO:0050783; P:cocaine metabolism; TAS.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLNESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC 3D-structure; Direct protein sequencing; Disease mutation;
CC Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.
CC SIGNAL 1 28
CC CHAIN 29 602 Cholinesterase.
CC ACT_SITE 226 226 Acyl-ester intermediate (By similarity).
CC ACT_SITE 353 353 Charge relay system (By similarity).
CC ACT_SITE 466 466 Charge relay system (By similarity).
CC DISULFID 93 120
CC DISULFID 280 291
CC DISULFID 428 547
CC DISULFID 599 599
CC CARBOHYD 45 45 Interchain.
CC CARBOHYD 85 85 N-linked (GlcNAc...)
CC CARBOHYD 134 134 N-linked (GlcNAc...)
CC CARBOHYD 269 269 N-linked (GlcNAc...)
CC CARBOHYD 284 284 N-linked (GlcNAc...)
CC CARBOHYD 369 369 N-linked (GlcNAc...)
CC CARBOHYD 483 483 N-linked (GlcNAc...)
CC CARBOHYD 509 509 N-linked (GlcNAc...)
CC CARBOHYD 514 514 N-linked (GlcNAc...)
CC VARIANT 98 98 D -> G (in atypical form, dibucaine-
CC resistant; dbSNP:1799807).
CC /FTId=VAR_002360.
CC T -> M (in fluoride-1).
CC VARIANT 271 271

```

FT VARIANT 358 358 /FTID=VAR_002361.
FT L -> I (in hypocholesterasemia).
FT /FTID=VAR_002362.
FT G -> V (in fluoride-2).
FT /FTID=VAR_002363.
FT A -> T (in K variant; with reduced enzyme
FT activity; dbSNP:1803274).
FT /FTID=VAR_002364.
SQ SEQUENCE 602 AA; 68418 MW; C9836409D9057F27 CRC64;

Query Match 71.3%; Score 62; DB 1; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.54;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 19
Q9N1N9 PRELIMINARY; PRT; 602 AA.
AC Q9N1N9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase (EC 3.1.1.8).
GN Name=BCHE;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20181263; PubMed=10718335; DOI=10.1016/S0006-2952(99)00389-5;
RA Wierdl M., Morton C.L., Danks M.K., Potter P.M.;
RT "Isolation and characterization of a cDNA encoding a horse liver
RT butyrylcholinesterase: evidence for CPT-11 drug activation.";
RL Biochem. Pharmacol. 59:773-781(2000).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DE EMBL; AF178685; AAF61480.1; -.
DR HSP; P06276; IPOF.
DR GO; GO:0004104; F:hydrolase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000397; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
FT CHAIN 1 29 Potential.
FT SIGNAL 30 603 butyrylcholinesterase.
SQ SEQUENCE 603 AA; 68480 MW; A350FDF68574ADF CRC64;

Query Match 71.3%; Score 62; DB 2; Length 603;
Best Local Similarity 64.3%; Pred. No. 0.54;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
| | | | | : | | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 21
CHLE_RABIT STANDARD; PRT; 581 AA.
ID CHLE_RABIT STANDARD; PRT; 581 AA.
AC P21927;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholesterase).
GN Name=BCHE;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand;
RX MEDLINE=90326526; PubMed=2374720;
RA Jbilo O., Roudani S., Chatonnet A.;
RT "Complete sequence of rabbit butyrylcholinesterase.";
RL Nucleic Acids Res. 18:3990-3990(1990).
RN [2]
RP SEQUENCE OF 75-215 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpagaus M., Chatonnet A., Maesson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 DR EMBL; X52090; CAA36308.1; --
 DR EMBL; X52091; CAA36308.1; JOINED.
 DR EMBL; X52092; CAA36308.1; JOINED.
 DR EMBL; M62779; AAA31169.1; --
 DR DR S10255; C39768.
 DR HSP; P22303; 1F8U
 DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Glycoprotein; Hydrolase; Serine esterase; Signal.
 FT SIGNAL 1 8
 FT CHAIN 9 581
 FT ACT_SITE 205 205 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 332 332 Charge relay system (By similarity).
 FT ACT_SITE 445 445 Charge relay system (By similarity).
 FT DISULFID 72 99 By similarity.
 FT DISULFID 259 270 By similarity.
 FT DISULFID 407 526 By similarity.
 FT DISULFID 578 578 Interchain (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 248 248 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 263 263 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 348 348 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 462 462 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 493 493 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 581 AA; 66156 MW; F88B199E7B32EB0A CRC64;

Query Match 70.1%; Score 61; DB 1; Length 581;
 Best Local Similarity 64.3%; Pred. No. 0.73; Indels 2; Gaps 0;
 Matches 9; Conservative 3; Mismatches 2;

Qy 1 AEFHRSSYVHWK 14

Db 552 AGFRHNNYMWAK 565

RESULT 22

CHLE_MOUSE
 ID CHLE_MOUSE STANDARD; PRT; 603 AA.
 AC Q03311;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudocholinesterase).
 GN Name=Bche;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90380429; PubMed=2400605; DOI=10.1016/0896-6273(90)90168-F;
 RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species.";
 RL Neuron 5:317-327 (1990).
 RN [2]
 RP SEQUENCE OF 97-237 FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=91201348; PubMed=2016308;
 RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
 RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 butyrylcholinesterase from several vertebrates.";
 RL J. Biol. Chem. 266:6966-6974 (1991).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
 CC two subunits in a dimer are linked by a disulfide bond.
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
 CC organophosphate esters.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; M99492; AAA37328.1; --
 DR PIR; S70849; S70849.
 DR HSP; P22303; 1F8U.
 DR MGI; MGI:894278; Bche.

DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR000997; Cholinesterase.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Glycoprotein; Hydrolase; Serine esterase; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 603
 FT ACT_SITE 227 227 Cholinesterase.
 FT ACT_SITE 354 354 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 467 467 Charge relay system (By similarity).
 FT DISULFID 94 121 Charge relay system (By similarity).
 FT DISULFID 281 292 By similarity.
 FT DISULFID 429 548 By similarity.
 FT DISULFID 600 600 Interchain (By similarity).
 FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 510 510 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 515 515 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 129 129 R -> P (in Ref. 2).
 SQ SEQUENCE 603 AA; 68521 MW; 719B1B2220D1E5367 CRC64;

Query Match 70.1%; Score 61; DB 1; Length 603;
 Best Local Similarity 64.3%; Pred. No. 0.76; Indels 2; Gaps 0;
 Matches 9; Conservative 3; Mismatches 2;

Qy 1 AEFHRSSYVHWK 14

Db 574 AGFRHNNYMWQ 587

RESULT 23

CHLE_FELCA
 ID CHLE_FELCA STANDARD; PRT; 602 AA.
 AC O62760;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)

```

DE (Pseudocholesterase).
GN Name=BCHE;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma.";
RL Biochem. Pharmacol. 60:479-487(2000).
CC -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond (By
CC similarity).
CC -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters (By similarity).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF053483; AAC06261.1; -.
DR HSSP; P22303; 1B41.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 602
FT ACT_SITE 226 226 Cholinesterase.
FT ACT_SITE 353 353 Acyl-ester intermediate (By similarity).
FT ACT_SITE 466 466 Charge relay system (By similarity).
FT DISULFID 93 120 By similarity.
FT DISULFID 280 291 By similarity.
FT DISULFID 428 547 Interchain (By similarity).
FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 269 269 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 483 483 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 602 AA; 68328 MW; EC8879232B74B9C CRC64;

Query Match 64.4%; Score 56; DB 1; Length 602;
Best Local Similarity 57.1%; Pred. No. 4.2;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 AEFHRWSSVMHWK 14
| : : : : :
Db 573 AGFYNNYMDWK 586

```

RESULT 24

```

CHLE_PANTT CHLE_PANTT STANDARD; PRT; 602 AA.
ID 062761;
AC 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholesterase).
GN Name=BCHE;
OS Panthera tigris tigris (Bengal tiger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
OX NCBI_TaxID=74535;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma.";
RL Biochem. Pharmacol. 60:479-487(2000).
CC -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond (By
CC similarity).
CC -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters (By similarity).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF053484; AAC06262.1; -.
DR HSSP; P22303; 1B41.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 602
FT ACT_SITE 226 226 Cholinesterase.
FT ACT_SITE 353 353 Acyl-ester intermediate (By similarity).
FT ACT_SITE 466 466 Charge relay system (By similarity).
FT DISULFID 93 120 By similarity.
FT DISULFID 280 291 By similarity.
FT DISULFID 428 547 Interchain (By similarity).
FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 269 269 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 483 483 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 602 AA; 68289 MW; EB0C8B9148E956A1 CRC64;

Query Match 64.4%; Score 56; DB 1; Length 602;
Best Local Similarity 57.1%; Pred. No. 4.2;

```

```
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AEFHRWSSYVHWK 14
Db 573 AGFYRWNNYMDWK 586

RESULT 25
Q8BJ7 PRELIMINARY; PRT; 205 AA.
AC Q8BJ7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein N (Fragment).
OS California encephalitis serogroup virus LEIV.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
OX NCBI_TaxID=178787;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2295875; PubMed=12408673;
RA Vanlandingham D.L., Davis B.S., Lvov S.D.,
RA Black W.C., Higgs S., Beaty B.J.;
RT "Molecular characterization of California serogroup viruses isolated
RT in Russia.";
RL Am. J. Trop. Med. Hyg. 67:306-309 (2002).
DR EMBL; AF392980; AAN60739.1; -.
DR GO; GO:0019013; C: viral nucleocapsid; IEA.
DR InterPro; IPR001784; Bunya_nucleocap.
DR Pfam; PF00952; Bunya_nucleocap; 1.
DR ProDom; PD001909; Bunya_nucleocap; 1.
FT NON TER 205
SQ SEQUENCE 205 AA; 23619 MW; 0A66C083F25A1491 CRC64;

Query Match 55.28; Score 48; DB 2; Length 205;
Best Local Similarity 60.08; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HRWSSYVHW 13
Db 93 HRWSSYVHW 102

RESULT 26
Q7RTL7 PRELIMINARY; PRT; 550 AA.
AC Q7RTL7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetylcholinesterase (EC 3.1.1.7) (Fragment).
GN Name=ache;
OS Ciona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=51511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2284560; PubMed=12396499; DOI=10.1098/rspb.2002.2122;
RA Weill M., Fort P., Berthomé eu A., Dubois M.P., Pasteur N.,
RA Raymond M.;
RT "A novel acetylcholinesterase gene in mosquitoes codes for the
RT insecticide target and is non-homologous to the ace gene in
RT Drosophila.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 269:2007-2016 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Fort P.P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000070; CAD29868.1; -.
```

```
DR HSPP; P21836; IJ07.
DR GO; GO:0003990; F: acetylcholinesterase activity; IEA.
DR GO; GO:0004104; F: cholinesterase activity; IEA.
DR GO; GO:0016787; F: hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
FT NON TER 1
SQ SEQUENCE 550 AA; 61942 MW; 4494459852A39C0A CRC64;

Query Match 54.08; Score 47; DB 2; Length 550;
Best Local Similarity 66.78; Pred. No. 83;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EFRWSSYVHW 13
Db 521 EFRWSSYVHW 532

RESULT 27
Q64NA7 PRELIMINARY; PRT; 667 AA.
AC Q64NA7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative helicase.
GN ORFNames=BF4288;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL; AP006841; BAD51028.1; -.
KW Helicase.
SQ SEQUENCE 667 AA; 76735 MW; 6DB01B9A729516C9 CRC64;

Query Match 53.48; Score 46.5; DB 2; Length 667;
Best Local Similarity 69.28; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 3 FHRWSSYVHWK 14
Db 405 FHRWSSYVHWK 417

RESULT 28
Q759Y3 PRELIMINARY; PRT; 709 AA.
AC Q759Y3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADR140CP.
GN ORFNames=ADR140C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RC STRAIN=ATCC 10895;
RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AE016817; AAS2060.1; -.
DR AGD; ADR140C; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
KW ATP-binding; Helicase; Hydrolase.
SQ SEQUENCE 709 AA; 78654 MW; 0B78934D3DF69F09 CRC64;

Query Match 51.7%; Score 45; DB 2; Length 709;
Best Local Similarity 35.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| : ||| : ||| :
Db 584 AQLHRYAAALLHWR 597

RESULT 29
Q857V6 PRELIMINARY; PRT; 143 AA.
AC Q857V6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp56.
OS Mycobacteriophage Cjw1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205869;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705966; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AY129331; AAN01670.1; -.
DR InterPro; IPR010982; Lambda like DNA.
SQ SEQUENCE 143 AA; 15905 MW; CECAD8876CBBF876 CRC64;

Query Match 50.6%; Score 44; DB 2; Length 143;
Best Local Similarity 46.2%; Pred. No. 64;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 13
| : ||| : ||| :
Db 11 ADDRWRSTVIDW 23

RESULT 30
Q78318 PRELIMINARY; PRT; 260 AA.
ID Q78318;
AC Q78318;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit F (Fragment).
GN Name=ndhf;
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99003705; PubMed=3787437;
RA Galloway G.L., Malmberg R.L., Price R.A.;
RT "Phylogenetic utility of the nuclear gene arginine decarboxylase: an
RT example from Brassicaceae";
RL Mol. Biol. Evol. 15:1312-1320(1998).
DR EMBL; AF064654; AAC68593.1; -.
DR PIR; T12393; T12393.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR InterPro; IPR003945; NADHpl_oxred5.
DR InterPro; IPR002128; Oxidored_q1_C.
DR Pfam; PF01010; Oxidored q1_C; 1.
DR PRINTS; PR01435; NPOXDRDTASE5.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 260 260
SQ SEQUENCE 260 AA; 30565 MW; 72E8DA2616AB9CF4 CRC64;

Query Match 50.6%; Score 44; DB 2; Length 260;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 FHRWSSYVHWK 14
| : ||| : ||| :
Db 192 FQKWSKRIHWE 203

RESULT 31
Q8HRN8 PRELIMINARY; PRT; 328 AA.
ID Q8HRN8;
AC Q8HRN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit F (fragment).
GN Name=ndhf;
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Hall J.C., Sytama K.J., Iltis H.H.;
RT "Phylogeny of Capparaceae and Brassicaceae based on chloroplast
RT sequence data.";
RL Am. J. Bot. 89:1826-1842(2002).
DR EMBL; AY122394; AAM82798.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009523; C:photosystem II; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR InterPro; IPR003945; NADHpl_oxred5.
DR InterPro; IPR002128; Oxidored q1_C.
DR Pfam; PF01010; Oxidored q1_C; 1.
DR PRINTS; PR01435; NPOXDRDTASE5.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 38091 MW; D762CACB85F262D0 CRC64;

Query Match 50.6%; Score 44; DB 2; Length 328;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 3 FHRWSSYVHWK 14
Db 278 FQKWSKRIHWE 289

RESULT 32
Q6YT37 PRELIMINARY; PRT; 357 AA.
AC Q6YT37
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leucine-rich repeat-containing 2.
GN Name=LRRC2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP006185; BAD08653.1; -.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR_1; 5.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00369; LRR_TYP; 4.
DR SEQUENCE 357 AA; 41468 MW; 3DF3C3DF0DE32E90 CRC64;

Query Match 50.6%; Score 44; DB 2; Length 357;
Best Local Similarity 47.4%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

Qy 2 EFHRWSSYVW-----HWK 14
Db 93 EGHKWSSEFVPELFGEHWK 111

RESULT 33
Q7S6U0 PRELIMINARY; PRT; 467 AA.
AC Q7S6U0
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU05499.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Galagan J.E., Cuomo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd K., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamayaselis M., Mauceli E., Bieleke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Navig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an

```

```

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AABX01000322; EAA31225.1; -.
DR HSPSP; Q93099; IRYB.
DR GO: 0004411; P:homogentisate 1,2-dioxygenase activity; IEA.
DR GO: 0006559; P:L-phenylalanine catabolism; IEA.
DR GO: 0006570; P:tyrosine metabolism; IEA.
DR InterPro: IPR005708; HmgA.
DR InterPro: IPR011051; RmlC_like_cupin.
DR Pfam: PF04209; Hgma; 1.
DR TIGRFAMs: TIGR01015; hmgA; 1.
KW Hypothetical protein.
SQ SEQUENCE 467 AA; 51560 MW; 21DB84436A32F316 CRC64;

Query Match 50.6%; Score 44; DB 2; Length 467;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HRWSSYVHWK 14
Db 444 HSWGKVHWK 454

RESULT 34
NUSC_ARATH STANDARD; PRT; 746 AA.
ID NUSC_ARATH
AC P56752; Q9MS93;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase
DE chain 5).
GN Name=ndhF; OrderedLocNames=AtG01010;
OS Arabidopsis thaliana (Mouse-ear Cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
RT thaliana.";
RL DNA Res. 6:283-290(1999).
RN [2]
RP SEQUENCE OF 18-426 FROM N.A.
RA Graham S.W., Reeves P.A., Burns A., Olmstead R.G.;
RA "Long branches in the seed plants and the root of the angiosperms.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone -> NAD(P)H +
CC plastoquinol.
CC -!- SIMILARITY: Belongs to the complex I subunit 5 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: AP000423; BAA84434.1; -.
CC EMBL: AF238049; AAF90035.1; -.
CC InterPro: IPR003945; NADHpl_oxred5.
CC InterPro: IPR003916; NADHpl_oxred5.
CC InterPro: IPR001750; Oxidored_q1.
CC InterPro: IPR002128; Oxidored_q1_C.
CC InterPro: IPR001516; Oxidored_q1_N.
CC Pfam: PF00361; Oxidored_q1; 1.

```

Pfam; PF01010; Oxidored q1_C; 1.
DR Pfam; PF00662; Oxidored q1_N; 1.
DR PRINTS; PRO1434; NADHDHGNASE5.
DR TIGRFAMs; TIGR01974; NDH I_L; 1.
KW Chloroplast; NAD; NADP; Oxidoreductase; Plastoquinone; Quinone.
SQ SEQUENCE 746 AA; 85238 MW; 1391A7875E9ETA29 CRC64;

Query Match 50.6%; Score 44; DB 1; Length 746;
Best Local Similarity 41.7%; Pred. No. 3.1e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FHRWSSYVHWK 14
| : | : | : ||:
Db 640 FQWNSKRIHWE 651

RESULT 35

Q94BA9 PRELIMINARY; PRT; 270 AA.

ID Q94BA9 AC Q94BA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Maturease K (Fragment).
DE Name=mak;
OS Rhagodia baccata (Coastal saltbush).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Rhagodia.
OX NCBI_TaxID=169240;
RN [1]
RP SEQUENCE FROM N.A.
RA Cuenoud P., Savolainen V., Chatrou L.W., Powell M., Grayer R.J.,
Chase M.W.;
RT "Molecular phylogenetics of Caryophyllales based on nuclear rDNA
and plastid rbcL, atpB, and matK DNA sequences.";
RL Am. J. Bot. 89:132-144(2002).
RR EMBL; AY042643; AAK94629.1; "-"
DR GO; GO:0008380; P-RNA splicing; IEA.
DR InterPro; IPRO08998; Agglutinin.
DR InterPro; IPRO00442; Intron_maturase2.
DR InterPro; IPRO02866; MatK_N.
DR Pfam; PF01348; Intron_maturas2; 1.
FT NON_TER 1
FT NON_TER 270 270
SQ SEQUENCE 270 AA; 32116 MW; 76375CF8CDC39FD0 CRC64;

Query Match 50.0%; Score 43.5; DB 2; Length 270;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 4 HRWSSYVHW-K 14
| : | : | : |:
Db 147 HKWKNYLIHFQW 158

RESULT 36

Q89Z67 PRELIMINARY; PRT; 651 AA.

ID Q89Z67 AC Q89Z67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative helicase.
DE OrderedLocusNames=B74510;
OS Bacteria; thetaiotomicron.
OC Bacteroides; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P.,
 RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J.J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RC Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC015598; AAI15598.1; -.
 DR HSSP; P02784; 1H8P.
 DR Genew; HGNC:14417; ELSPBP1.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00040; fn2; 4.
 DR PRINTS; PR00013; FNTYPEII.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 4.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 SQ SEQUENCE 223 AA; 26105 MW; F29CCF5BA3E5CE51 CRC64;

 Query Match 49.4%; Score 43; DB 2; Length 223;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps

 Qy 5 RWSSYVWVH 13
 Db 3 RWSYLLGW 11
 |||||:|
 |||||:

 RESULT 41
 Q96RT0 PRELIMINARY; PRT; 223 AA.
 AC Q96RT0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Seminal plasma protein-like protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Luo Y., Zhang X., Yu B.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF279147; AAK69481.1; -.
 DR HSSP; P02784; 1H8P.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00040; fn2; 4.
 DR PRINTS; PR00013; FNTYPEII.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 4.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 SQ SEQUENCE 223 AA; 26077 MW; F29CD04BA3E5CE51 CRC64;

 Query Match 49.4%; Score 43; DB 2; Length 223;

```

Best Local Similarity 66.7%; Pred. NO. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RWSSVMVHM 13
DB 3 RWSYLLGW 11

RESULT 42
Q9LMW9 PRELIMINARY; PRT; 392 AA.
ID Q9LMW9
AC Q9LMW9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE F5M15.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
RA Lenz C., Li J., Liu A., Liu K., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC027665; AAF79601.1; -.
DR InterPro; IPR006527; F_box_assoc_1.
DR TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
SQ SEQUENCE 392 AA; 44526 MW; A8135F563D904EEB CRC64;

Query Match 49.4%; Score 43; DB 2; Length 392;
Best Local Similarity 50.0%; Pred. NO. 2.3e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 AEFHRWSSVMV----HWK 14
DB 298 AEKHQWSSYIVLPPPWK 315

RESULT 43
Q9LM89 PRELIMINARY; PRT; 422 AA.
ID Q9LM89
AC Q9LM89;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE F2D10.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC027665; AAF79601.1; -.
DR InterPro; IPR006527; F_box_assoc_1.
DR TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
SQ SEQUENCE 392 AA; 44526 MW; A8135F563D904EEB CRC64;

Query Match 49.4%; Score 43; DB 2; Length 392;
Best Local Similarity 50.0%; Pred. NO. 2.3e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 AEFHRWSSVMV----HWK 14
DB 298 AEKHQWSSYIVLPPPWK 315

RESULT 44
SMP3_YEAST STANDARD; PRT; 516 AA.
ID SMP3_YEAST
AC Q04174; Q99400;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE SMP3 protein.
GN Name=SMP3; OrderedLocusNames=YOR149C;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NBW5;
RX MEDLINE=91172125; PubMed=2005867;
RA Irie K., Araki H., Oshima Y.;
RT "Mutations in a Saccharomyces cerevisiae host showing increased
RT holding stability of the heterologous plasmid pSR1.";
RL Mol. Gen. Genet. 225:257-265(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1678;
RX PubMed=9046089;
RX DOI=10.1002/(SICI)1097-0061(199701)13:1<73::AID-YEA52>3.3.CO;2-D;
RA Bordonne R., Camasses A., Madania A., Poch O., Tarasov I., Winsor B.,
RA Martin R.P.;
RT "Analysis of a 35.6 kb region on the right arm of Saccharomyces
RT cerevisiae chromosome XV.";
RL Yeast 13:73-83(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313270; PubMed=9169874;
RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansoorge W.,
RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
RA Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,
RA Cziepluch C., Daignan-Fornier B., Dang D.V., de Haan M., Delius H.,
RA Durand P., Fairhead C.A., Feldmann H., Gallon L., Galisson F.,
RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,

```

```

RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Cheuk R., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howng B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC069251; AAF80636.1; -.
DR PIR; D86339; D86339.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006527; F_box_assoc_1.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
SQ SEQUENCE 422 AA; 48016 MW; 7D02BC286346BC52 CRC64;

Query Match 49.4%; Score 43; DB 2; Length 422;
Best Local Similarity 50.0%; Pred. NO. 2.5e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 AEFHRWSSVMV----HWK 14
DB 328 AEKHQWSSYIVLPPPWK 345

RESULT 44
SMP3_YEAST STANDARD; PRT; 516 AA.
ID SMP3_YEAST
AC Q04174; Q99400;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE SMP3 protein.
GN Name=SMP3; OrderedLocusNames=YOR149C;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NBW5;
RX MEDLINE=91172125; PubMed=2005867;
RA Irie K., Araki H., Oshima Y.;
RT "Mutations in a Saccharomyces cerevisiae host showing increased
RT holding stability of the heterologous plasmid pSR1.";
RL Mol. Gen. Genet. 225:257-265(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1678;
RX PubMed=9046089;
RX DOI=10.1002/(SICI)1097-0061(199701)13:1<73::AID-YEA52>3.3.CO;2-D;
RA Bordonne R., Camasses A., Madania A., Poch O., Tarasov I., Winsor B.,
RA Martin R.P.;
RT "Analysis of a 35.6 kb region on the right arm of Saccharomyces
RT cerevisiae chromosome XV.";
RL Yeast 13:73-83(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313270; PubMed=9169874;
RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansoorge W.,
RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
RA Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,
RA Cziepluch C., Daignan-Fornier B., Dang D.V., de Haan M., Delius H.,
RA Durand P., Fairhead C.A., Feldmann H., Gallon L., Galisson F.,
RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,

```

RA Habbig B., Hand N.J., Hani J., Hattenhorst U., Hebling U.,
RA Hernando Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,
RA Hollenberg C.P., Hughes E., Jauniaux J.-C., Kaloeropoulos A.,
RA Katsoulou C., Kordes E., Lafuente M.J., Landt O., Louis E.J.,
RA Maarse A.C., Madania A., Mannhaupt G., Marck C., Martin R.P.,
RA Mewes H.-W., Michaux G., Paces V., Parle-McDermott A.G., Pearson B.M.,
RA Perrat A., Petterson B., Poch O., Pohl T.M., Poirey R.,
RA Portetle D., Fajol A., Fumelle B., Ramezani Rad M., Rechmann S.,
RA Schwager C., Schweizer M., Sor F., Sterky F., Tarasov I.A.,
RA Tedoru C., Tetzelin H., Thierry A., Tobiasch E., Tzermia M.,
RA Uhlen M., Unsel M., Valens M., Vandenbol M., Vetter I., Vleck C.,
RA Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Wiemann S.,
RA Winsor B., Wolfe K.H., Zollner A., Zumstein E., Kleine K.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";
RL Nature 387:98-102(1997).
CC -!- FUNCTION: Essential protein involved in plasmid maintenance with
CC SMP2.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: To S.pombe SPAC4G8.12c.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X58121; CAA41123.1; -;
CC EMBL: U55020; AAC49635.1; -;
CC EMBL: Z75057; CAA99355.1; -;
CC PIR: S67037; S67037.
CC
CC GermOnline; 143737; -;
CC SGD: S000005675; SMP3.
CC GO: GO:0006276; P:plasmid maintenance; IMP.
CC InterPro: IPR005599; Alg9 trans.
CC Pfam: PF03901; Glyco_transf_22; 1.
KW Transmembrane.
FT TRANSMEM 6 26 Potential.
FT TRANSMEM 61 81 Potential.
FT TRANSMEM 176 196 Potential.
FT TRANSMEM 211 231 Potential.
FT TRANSMEM 271 291 Potential.
FT TRANSMEM 296 316 Potential.
FT TRANSMEM 318 338 Potential.
FT TRANSMEM 349 369 Potential.
FT TRANSMEM 122 123 MQ -> IK (in Ref. 1).
FT CONFLICT 163 163 E -> G (in Ref. 1).
FT CONFLICT 169 169 S -> R (in Ref. 1).
FT CONFLICT 279 279 V -> L (in Ref. 1).
SQ SEQUENCE 516 AA; 59900 MW; 8D8404622CB69534 CRC64;

Query Match 49.4%; Score 43; DB 1; Length 516;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 WSSYVHVHK 14
DB 204 WKFYRVHVK 212

RESULT 45
Q95T11 PRELIMINARY; PRT; 564 AA.
AC Q95T11
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SD02533p.
GN Name=a22;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokatein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY058758; AAL13987.1; -;
DR FlyBase: FBgn0025185; a22.
DR GO: GO:0005334; C:nucleus; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR InterPro: IPR000215; Prot inh serpin.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF00096; zf-C2H2; 7.
DR SMART: SM00355; Znf_C2H2; 7.
DR PROSITE: PS00284; SERPIN; UNKNOWN 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 7.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 6.
SQ SEQUENCE 564 AA; 65530 MW; 15CE998366CE19D6 CRC64;

Query Match 49.4%; Score 43; DB 2; Length 564;
Best Local Similarity 53.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFHRWSSYVHVHK 14
DB 2 EFHRWREFIVHVK 14

Search completed: October 12, 2005, 10:19:56
Job time : 77 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:06:29 ; Search time 15 Seconds

(without alignments)
89.802 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

PIR 79.*

1: piri.*

2: piri2.*

3: piri3.*

4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	583	2 S10712	acetylcholinestera
2	87	100.0	584	2 S48724	acetylcholinestera
3	87	100.0	614	2 A39256	acetylcholinestera
4	87	100.0	614	2 JH0314	acetylcholinestera
5	87	100.0	614	2 JH0811	acetylcholinestera
6	80	92.0	599	1 A38868	acetylcholinestera
7	80	92.0	599	1 A38868	acetylcholinestera
8	65	74.7	767	2 S47639	acetylcholinestera
9	62	71.3	602	1 ACHU	cholinesterase (EC
10	61	70.1	581	2 C39768	cholinesterase (EC
11	61	70.1	603	2 S70849	cholinesterase (EC
12	44	50.6	260	2 T12393	NADH2 dehydrogenas
13	43	49.4	422	2 D86339	protein F2D10.14 [
14	43	49.4	516	2 S67037	SMP3 protein - yea
15	42	48.3	100	2 A87273	conserved hypotet
16	42	48.3	1792	2 T08878	supervillin P205 -
17	41	47.1	290	2 C96911	transcription regu
18	41	47.1	397	2 A75137	hypothetical prote
19	41	47.1	512	2 F96741	probable sucrose t
20	41	47.1	523	2 A97177	site-specific reco
21	41	47.1	535	2 B83936	hypothetical prote
22	41	47.1	818	2 H83904	hypothetical prote
23	41	47.1	1323	2 T30253	spalt protein - mo
24	40.5	46.6	510	1 S64059	stearyl-CoA 9-des
25	40	46.0	90	2 PH1152	Ig heavy chain V r
26	40	46.0	184	2 JC2152	hypothetical 20.8K
27	40	46.0	211	2 B84035	hypothetical prote
28	40	46.0	245	2 S48351	hypothetical prote
29	40	46.0	450	2 A64546	hypothetical prote

30	40	46.0	1350	2 T30341	zinc finger protei
31	40	46.0	1995	2 T08166	probable membrane
32	39.5	45.4	469	2 S74825	probable Rieske ir
33	39.5	45.4	542	2 T02379	hypothetical prote
34	39	44.8	100	2 T09856	sucrose synthase (
35	39	44.8	138	1 HVMST7	Ig heavy chain pre
36	39	44.8	199	2 B82315	hypothetical prote
37	39	44.8	226	2 S37434	membrane glycoprot
38	39	44.8	226	2 D49591	membrane protein M
39	39	44.8	259	2 T12386	NADH2 dehydrogenas
40	39	44.8	260	2 T12395	NADH2 dehydrogenas
41	39	44.8	260	2 T12394	NADH2 dehydrogenas
42	39	44.8	260	2 T14435	NADH2 dehydrogenas
43	39	44.8	272	2 F89904	glycerol uptake fa
44	39	44.8	408	2 D83191	conserved hypotet
45	39	44.8	507	2 B42249	serine-type carbox
46	39	44.8	524	2 T04564	cytochrome P450 ho
47	39	44.8	526	2 T04566	cytochrome P450 ho
48	39	44.8	618	2 S33044	hypothetical prote
49	39	44.8	651	2 F89798	hypothetical prote
50	39	44.8	1237	2 T37529	hypothetical prote
51	38.5	44.3	196	2 AB2265	hypothetical prote
52	38.5	44.3	277	2 G89833	teichoic acid tran
53	38.5	44.3	287	2 T04236	xyloglucan endo-1,
54	38.5	44.3	907	2 AB1885	hypothetical prote
55	38	43.7	58	2 D49038	Ig lambda chain V
56	38	43.7	117	2 S01185	NADH2 dehydrogenas
57	38	43.7	117	2 G25797	NADH2 dehydrogenas
58	38	43.7	119	2 S20640	Ig heavy chain V r
59	38	43.7	122	2 S32185	Ig heavy chain V r
60	38	43.7	157	2 G82214	hypothetical prote
61	38	43.7	166	2 PL0012	Ig heavy chain pre
62	38	43.7	237	2 G90486	hypothetical prote
63	38	43.7	239	2 C97372	hypothetical prote
64	38	43.7	239	2 AB2590	conserved hypotet
65	38	43.7	267	2 B86313	hypothetical prote
66	38	43.7	285	2 E70707	hypothetical prote
67	38	43.7	298	2 AF0578	CitG protein [lipo
68	38	43.7	302	2 A95371	probable LygR-fami
69	38	43.7	351	1 SAVZVW	surface antigen pr
70	38	43.7	351	1 SAVZWR	surface antigen pr
71	38	43.7	353	1 SAVZVC	surface antigen pr
72	38	43.7	358	2 AB1746	hypothetical prote
73	38	43.7	379	2 T32778	hypothetical prote
74	38	43.7	591	2 B82429	polyhydroxyalkanoi
75	38	43.7	612	2 F83000	probable two-compo
76	38	43.7	619	2 B87682	hypothetical prote
77	38	43.7	650	2 S23217	beta-fructofuranos
78	38	43.7	710	2 G82689	soluble lytic mure
79	38	43.7	1234	2 A34911	band 3-related pro
80	38	43.7	1237	2 A56764	band 3-related pro
81	38	43.7	1237	2 A31789	band 3-related pro
82	38	43.7	1239	1 A32579	neuroglian - fruit
83	38	43.7	2924	2 T18378	variant-specific a
84	38	43.7	3026	2 T28431	variant surface pr
85	38	43.7	3078	2 T28432	variant-specific a
86	37.5	43.1	285	2 S72787	hypothetical prote
87	37.5	43.1	333	2 S52960	NADH2 dehydrogenas
88	37.5	43.1	494	2 A48285	exopolysphatase
89	37.5	43.1	494	2 H91217	guanosine pentapho
90	37.5	43.1	494	2 A86064	guanosine pentapho
91	37	42.5	71	2 PH1136	Ig heavy chain V r
92	37	42.5	96	2 S17606	Ig heavy chain V r
93	37	42.5	97	2 S26895	Ig heavy chain V r
94	37	42.5	109	2 S68171	Ig lambda chain V
95	37	42.5	111	2 S25033	Ig heavy chain V r
96	37	42.5	111	2 S25034	Ig heavy chain V r
97	37	42.5	119	2 S03077	Ig heavy chain V r
98	37	42.5	137	1 G2MS43	Ig heavy chain pre
99	37	42.5	162	2 T17049	NADH2 dehydrogenas
100	37	42.5	162	2 AB1950	hypothetical prote
101	37	42.5	185	2 S48943	hypothetical prote
102	37	42.5	222	2 S55294	conserved hypotet

103	37	42.5	228	2	AB3098	hypothetical prote	176	36	41.4	326	2	T38706	hypothetical prote
104	37	42.5	240	2	C87409	hypothetical prote	177	36	41.4	396	2	A71134	hypothetical prote
105	37	42.5	246	2	B97752	hypothetical prote	178	36	41.4	397	2	C91007	probable salicylat
106	37	42.5	259	2	B72505	hypothetical prote	179	36	41.4	397	2	E85851	probable hydroxyla
107	37	42.5	285	2	S55960	probable membrane	180	36	41.4	470	2	T47926	hypothetical prote
108	37	42.5	299	2	AC0794	conserved hypothet	181	36	41.4	475	2	C72538	probable cysteinyl
109	37	42.5	321	2	S59388	probable membrane	182	36	41.4	509	2	C94858	probable citrate s
110	37	42.5	328	1	DEHUE7	estradiol 17beta-d	183	36	41.4	516	2	E70779	probable glp1 pro
111	37	42.5	345	2	T24659	hypothetical prote	184	36	41.4	523	2	T22728	hypothetical prote
112	37	42.5	389	2	E90431	lipid biosynt	185	36	41.4	527	2	H85135	hypothetical prote
113	37	42.5	438	2	B11963	probable outer mem	186	36	41.4	537	2	F70758	hypothetical prote
114	37	42.5	459	2	G82891	hypothetical prote	187	36	41.4	546	1	C70393	probable adenylyl-
115	37	42.5	506	2	F83545	hypothetical prote	188	36	41.4	570	2	F71049	glutamine-tRNA lig
116	37	42.5	552	2	T08148	proline-rich myros	189	36	41.4	575	1	JC5432	glycoprotein 6-alp
117	37	42.5	662	2	A33481	interferon-induced	190	36	41.4	578	1	F64578	oligoendopeptidase
118	37	42.5	676	2	T01092	cullin-like protei	191	36	41.4	578	2	B71934	oligopeptidase - H
119	37	42.5	686	2	S30075	ferric reductase (192	36	41.4	578	2	AC5810	alpha,alpha-trehal
120	37	42.5	871	2	T34427	pob1 protein - fis	193	36	41.4	583	2	JC6504	alpha,alpha-trehal
121	37	42.5	891	2	T29561	hypothetical prote	194	36	41.4	602	2	T22805	hypothetical prote
122	37	42.5	1096	2	C87263	hypothetical prote	195	36	41.4	608	2	T22804	hypothetical prote
123	37	42.5	1332	2	T15670	hypothetical prote	196	36	41.4	630	1	G64226	hypothetical prote
124	37	42.5	1350	2	S00647	finger protein - A	197	36	41.4	643	2	T33940	hypothetical prote
125	37	42.5	1357	2	S57052	hypothetical prote	198	36	41.4	643	2	S55593	membrane protein S
126	37	42.5	2240	2	T37057	probable multi-dom	199	36	41.4	654	2	S69673	SAC7 protein - yea
127	36.5	42.0	84	2	T51757	hypothetical prote	200	36	41.4	669	2	T13335	hypothetical prote
128	36.5	42.0	125	2	AE0562	probable membrane	201	36	41.4	669	2	T13640	probable minor str
129	36.5	42.0	186	2	T50361	hypothetical prote	202	36	41.4	698	2	T21781	hypothetical prote
130	36.5	42.0	290	2	B97100	pyridoxal kinase r	203	36	41.4	700	2	S09699	bib protein - frui
131	36.5	42.0	316	2	T19435	hypothetical prote	204	36	41.4	734	1	S26072	photosystem I prot
132	36.5	42.0	372	2	F70467	hypothetical prote	205	36	41.4	737	2	T06839	probable photost
133	36.5	42.0	1407	2	B42239	adenylate cyclase	206	36	41.4	751	2	AG1999	(p)ppgp 3-pyropho
134	36	41.4	40	2	S33407	Ig heavy chain v r	207	36	41.4	755	2	T47806	hypothetical prote
135	36	41.4	94	2	PH0996	Ig heavy chain v r	208	36	41.4	758	2	S36711	dolichyl-phosphate
136	36	41.4	96	2	S17617	Ig heavy chain v r	209	36	41.4	758	2	D71072	hypothetical prote
137	36	41.4	96	2	S17618	Ig heavy chain v r	210	36	41.4	765	2	C75100	hypothetical prote
138	36	41.4	97	2	PH17603	Ig heavy chain v r	211	36	41.4	766	2	B75059	probable transmem
139	36	41.4	98	2	PH1111	Ig heavy chain v r	212	36	41.4	829	2	S58888	Ins P4-binding pro
140	36	41.4	98	2	PH1147	Ig heavy chain v r	213	36	41.4	829	2	S71847	Ins P4-binding pro
141	36	41.4	98	2	S26313	Ig heavy chain v r	214	36	41.4	848	2	T25325	hypothetical prote
142	36	41.4	98	2	S26312	Ig heavy chain v r	215	36	41.4	995	2	H59432	RhoGAP protein hom
143	36	41.4	101	2	S26311	Ig heavy chain v r	216	36	41.4	1117	2	A38227	RNA-splicing regul
144	36	41.4	101	2	S26310	Ig heavy chain v r	217	36	41.4	1256	2	S60461	gene flightless-I
145	36	41.4	104	2	S26466	Ig heavy chain v r	218	36	41.4	1420	2	A32869	apolipoprotein(a)
146	36	41.4	104	2	PH0991	Ig heavy chain v r	219	36	41.4	1423	2	A49206	exo-beta-D-fructos
147	36	41.4	106	2	F32513	Ig heavy chain v r	220	36	41.4	4548	1	S00657	apoptin(a) (EC
148	36	41.4	109	2	PH0989	Ig heavy chain v r	221	36	41.4	8243	2	T31307	type I fatty acid
149	36	41.4	109	2	PH1094	Ig heavy chain v r	222	35.5	40.8	80	2	C82809	hypothetical prote
150	36	41.4	109	2	PH1096	Ig heavy chain v r	223	35.5	40.8	272	2	AB3430	transposase BME114
151	36	41.4	110	2	PH0995	Ig heavy chain v r	224	35.5	40.8	278	2	AG2176	hypothetical prote
152	36	41.4	111	2	PH0993	Ig heavy chain v r	225	35.5	40.8	406	2	AG0548	probable ABC-trans
153	36	41.4	111	2	PH0994	Ig heavy chain v r	226	35.5	40.8	411	2	S46800	LAG1 protein - yea
154	36	41.4	111	2	PH0992	Ig heavy chain v r	227	35.5	40.8	412	2	F69796	sugar-binding prot
155	36	41.4	112	2	S26473	Ig heavy chain v r	228	35.5	40.8	418	2	S30134	hypothetical prote
156	36	41.4	123	2	C87662	IS298, transposase	229	35.5	40.8	493	2	AH0922	guanosine-5'-triph
157	36	41.4	125	2	S20639	Ig heavy chain v r	230	35.5	40.8	515	2	F88618	protein W06F12.2 l
158	36	41.4	131	2	S66537	Ig heavy chain v r	231	35.5	40.8	562	2	T26242	hypothetical prote
159	36	41.4	138	2	S21810	Ig heavy chain v r	232	35.5	40.8	568	2	T26243	hypothetical prote
160	36	41.4	156	2	E84197	hypothetical prote	233	35.5	40.8	1074	2	G56504	probable En/spm-li
161	36	41.4	193	2	T34047	hypothetical prote	234	35.5	40.8	1121	2	F86485	hypothetical prote
162	36	41.4	196	2	T29016	hypothetical prote	235	35.5	40.8	1426	2	E90456	oxydoreductase, pr
163	36	41.4	210	2	A82411	probable methyltra	236	35	40.2	35	2	S46472	Ig heavy chain v r
164	36	41.4	211	2	PC4202	monoclonal antibod	237	35	40.2	35	2	S26887	Ig heavy chain v r
165	36	41.4	221	2	T27980	hypothetical prote	238	35	40.2	35	2	S46473	Ig heavy chain v r
166	36	41.4	228	2	D90620	cytochrome c oxida	239	35	40.2	94	2	S20653	Ig heavy chain v r
167	36	41.4	260	2	T12391	NADH2 dehydrogenas	240	35	40.2	94	2	S20650	Ig heavy chain v r
168	36	41.4	260	2	T12387	NADH2 dehydrogenas	241	35	40.2	94	2	PL0120	Ig heavy chain v r
169	36	41.4	260	2	T12390	NADH2 dehydrogenas	242	35	40.2	96	2	C33730	Ig heavy chain v r
170	36	41.4	260	2	T12392	NADH2 dehydrogenas	243	35	40.2	97	2	S26885	Ig heavy chain v r
171	36	41.4	272	2	AC1267	glycerol uptake fa	244	35	40.2	97	2	S26886	Ig heavy chain v r
172	36	41.4	272	2	AE1629	glycerol uptake fa	245	35	40.2	97	2	S54855	Ig heavy chain v r
173	36	41.4	276	2	T16523	hypothetical prote	246	35	40.2	98	2	PL0121	Ig heavy chain v r
174	36	41.4	288	2	S41194	transmembrane prot	247	35	40.2	98	2	S29545	Ig heavy chain v r
175	36	41.4	308	2	JC5468	leukocidin chain 1	248	35	40.2	98	2	S29546	Ig heavy chain v r

249	35	40.2	98	2	S26896	Ig heavy chain v r	322	35	40.2	527	2	T25131	hypothetical prote
250	35	40.2	98	2	PH1061	Ig light chain v r	323	35	40.2	529	1	SAHU4F	cell surface antig
251	35	40.2	99	2	C48223	Ig heavy chain v r	324	35	40.2	533	2	T10216	hypothetical prote
252	35	40.2	101	2	PH1021	Ig heavy chain v r	325	35	40.2	549	1	S39533	phosphoprotein pho
253	35	40.2	105	2	PH1020	Ig heavy chain v r	326	35	40.2	553	2	A88495	protein C0688.4 [i
254	35	40.2	109	2	PH1653	Ig heavy chain v r	327	35	40.2	553	2	H88671	protein P28E10.3 [
255	35	40.2	109	2	PH1646	Ig heavy chain v r	328	35	40.2	553	2	T23244	hypothetical prote
256	35	40.2	109	2	PH1644	Ig heavy chain v r	329	35	40.2	553	2	T21233	hypothetical prote
257	35	40.2	111	2	PH1019	Ig heavy chain v r	330	35	40.2	553	2	T24639	hypothetical prote
258	35	40.2	111	2	PH1645	Ig heavy chain v r	331	35	40.2	553	2	A89723	protein F47C8.1 [i
259	35	40.2	111	2	S69475	hypothetical prote	332	35	40.2	555	2	S27163	alpha, alpha-trehal
260	35	40.2	112	2	PH1022	Ig heavy chain v r	333	35	40.2	560	2	E96554	hypothetical prote
261	35	40.2	114	2	S46390	Ig heavy chain v r	334	35	40.2	562	2	G70180	serine/threonine k
262	35	40.2	114	2	S46391	Ig heavy chain v r	335	35	40.2	575	2	AG2566	hypothetical prote
263	35	40.2	114	2	S46392	Ig heavy chain v r	336	35	40.2	585	2	T18885	hypothetical prote
264	35	40.2	114	2	S20707	Ig heavy chain v r	337	35	40.2	589	2	I38598	zinc finger protei
265	35	40.2	116	2	S12557	Ig heavy chain - h	338	35	40.2	594	2	T22072	hypothetical prote
266	35	40.2	116	2	S22558	Ig heavy chain v r	339	35	40.2	596	2	T23084	hypothetical prote
267	35	40.2	117	2	S36270	Ig heavy chain v r	340	35	40.2	607	2	T23085	hypothetical prote
268	35	40.2	118	2	S31677	Ig heavy chain v r	341	35	40.2	625	2	S68633	hypothetical prote
269	35	40.2	118	2	S38717	Ig heavy chain v r	342	35	40.2	625	2	T32739	hypothetical prote
270	35	40.2	119	2	F36005	Ig heavy chain v r	343	35	40.2	626	2	AE0123	probable antigenic
271	35	40.2	120	2	S31112	Ig heavy chain - h	344	35	40.2	629	2	T22066	hypothetical prote
272	35	40.2	121	2	S20783	Ig heavy chain v r	345	35	40.2	633	2	T21779	hypothetical prote
273	35	40.2	121	2	G36005	Ig heavy chain v r	346	35	40.2	634	2	S77096	icfg protein slx18
274	35	40.2	122	2	S36005	Ig heavy chain v r	347	35	40.2	637	2	H96592	probable multisp
275	35	40.2	123	2	S38493	Ig heavy chain - h	348	35	40.2	639	2	T50793	hypothetical prote
276	35	40.2	134	2	S31679	Ig heavy chain v r	349	35	40.2	644	2	T22067	hypothetical prote
277	35	40.2	137	2	S31701	Ig heavy chain v r	350	35	40.2	649	2	H86920	probable membrane
278	35	40.2	137	2	T17048	NADH2 dehydrogen	351	35	40.2	658	2	T32893	hypothetical prote
279	35	40.2	169	2	D84027	molybdopterin-gua	352	35	40.2	659	2	D84633	probable multisp
280	35	40.2	212	2	D64662	biotin operon repr	353	35	40.2	661	2	T20877	hypothetical prote
281	35	40.2	215	2	E84078	hypothetical prote	354	35	40.2	662	2	T44219	hypothetical prote
282	35	40.2	224	2	AD3278	nicotinamide-nucle	355	35	40.2	662	2	T31986	hypothetical prote
283	35	40.2	225	2	A88991	protein C36C5.3 [i	356	35	40.2	669	2	T24571	hypothetical prote
284	35	40.2	235	1	VHVVUV	nucleoprotein N -	357	35	40.2	670	2	T09205	hypothetical prote
285	35	40.2	235	1	VHVUNH	nucleoprotein N -	358	35	40.2	670	2	T09274	hypothetical prote
286	35	40.2	250	2	F75219	hypothetical prote	359	35	40.2	670	2	T32221	hypothetical prote
287	35	40.2	255	2	T24406	hypothetical prote	360	35	40.2	671	2	B75607	conserved hypothet
288	35	40.2	259	2	T15841	hypothetical prote	361	35	40.2	677	2	T23083	hypothetical prote
289	35	40.2	264	2	I39696	beta-lactamase (EC	362	35	40.2	682	2	T22064	hypothetical prote
290	35	40.2	268	2	F86678	sugar hydrolase [i	363	35	40.2	685	2	T32571	hypothetical prote
291	35	40.2	279	2	T16816	hypothetical prote	364	35	40.2	689	2	T25202	hypothetical prote
292	35	40.2	279	2	T16425	hypothetical prote	365	35	40.2	692	2	T28783	hypothetical prote
293	35	40.2	279	2	T15313	hypothetical prote	366	35	40.2	695	2	T28782	hypothetical prote
294	35	40.2	297	2	T24718	hypothetical prote	367	35	40.2	699	2	A82425	helicase IV VCA071
295	35	40.2	299	2	A70713	hypothetical prote	368	35	40.2	734	2	T07280	photosystem I P700
296	35	40.2	304	2	T34475	hypothetical prote	369	35	40.2	735	2	S41481	P700 chlorophyll a
297	35	40.2	318	2	JC6115	gamma-glutamyl hyd	370	35	40.2	761	2	H84950	ribonucleoside-dip
298	35	40.2	319	2	D89778	hypothetical prote	371	35	40.2	775	2	T22200	hypothetical prote
299	35	40.2	325	2	T31989	hypothetical prote	372	35	40.2	780	2	T39057	hypothetical prote
300	35	40.2	330	2	S53990	DNA methyltransfer	373	35	40.2	790	2	T24354	hypothetical prote
301	35	40.2	336	2	C71964	UDP-3-O-[3-hydroxy	374	35	40.2	805	2	C87861	protein F43G9.7 [i
302	35	40.2	336	2	D64544	UDP-3-O-[3-hydroxy	375	35	40.2	805	2	T32377	hypothetical prote
303	35	40.2	355	2	C96007	probable ornithine	376	35	40.2	815	2	T00264	high carbon dioxid
304	35	40.2	359	2	AE0541	probable fibrillar	377	35	40.2	838	2	B38656	vacuolar proton pu
305	35	40.2	373	2	S55718	interleukin-2 rece	378	35	40.2	874	2	H86167	hypothetical prote
306	35	40.2	377	2	S6047n	probable 1-acyl-n	379	35	40.2	891	2	T28828	hypothetical prote
307	35	40.2	388	2	F83738	hypothetical prote	380	35	40.2	919	2	T21049	hypothetical prote
308	35	40.2	389	2	C82130	conserved hypothet	381	35	40.2	1013	2	T16244	hypothetical prote
309	35	40.2	393	2	T12492	hypothetical prote	382	35	40.2	1025	2	H86250	hypothetical prote
310	35	40.2	397	2	F70001	multidrug resistan	383	35	40.2	1050	2	G70396	cation efflux gyst
311	35	40.2	415	2	B84544	probable WD-40 rep	384	35	40.2	1174	2	H44982	exodeoxyribonuclea
312	35	40.2	448	2	T15589	hypothetical prote	385	35	40.2	1188	2	S48861	gene e1 protein -
313	35	40.2	449	2	JQ0172	tubulin beta chain	386	35	40.2	1227	2	A33638	erythrocyte anion
314	35	40.2	457	2	JQ2184	hypothetical 50.4K	387	35	40.2	1227	2	B34911	band 3-related pro
315	35	40.2	466	2	F85913	hypothetical prote	388	35	40.2	1232	2	T38496	anion exchanger 3
316	35	40.2	466	2	D91069	hypothetical prote	389	35	40.2	1319	2	H84542	hypothetical prote
317	35	40.2	466	2	H65045	gamma-aminobutyrat	390	35	40.2	1458	1	A49707	phospholipase A2 r
318	35	40.2	471	2	T34956	probable UDP-N-ace	391	35	40.2	1463	2	A53210	phospholipase A2 r
319	35	40.2	494	2	T09289	nicotinic acetylch	392	35	40.2	1493	2	F70435	glutamate synthase
320	35	40.2	494	2	S22324	replication initia	393	35	40.2	2025	2	T21588	hypothetical prote
321	35	40.2	516	2	S53007	citrate synthase -	394	35	40.2	2228	2	T14029	variant-specific s

C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein
 F;32-538/Domain: cholinesterase homology <CHE>
 F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;203/Active site: Ser #status predicted

Query Match 100.0%; Score 87; DB 2; Length 583;
 Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
 |||||
 Db 555 AEFHRWSSVMVHWK 568

RESULT 2

S48724
 acetylcholinesterase - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
 C;Accession: S48724
 R;Jbilo, O.; L'Hermite, Y.; Tulesa, V.; Toutant, J.P.; Chatonnet, A.
 Eur. J. Biochem. 225, 115-124, 1994
 A;Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue
 A;Reference number: S48724; MUID:95010096; PMID:7925428
 A;Accession: S48724
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-584 <JBI>
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: glycoprotein
 F;32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 584;
 Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
 |||||
 Db 556 AEFHRWSSVMVHWK 569

RESULT 3

A39256
 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
 C;Species: Homo sapiens (man)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
 C;Accession: A39256; S03959
 R;Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Ghatt, A.; Neville, L.; Lieman-Hurw
 Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
 A;Title: Molecular cloning and construction of the coding region for human acetylcholine
 A;Reference number: A39256; MUID:91088577; PMID:2263619
 A;Accession: A39256
 A;Molecule type: mRNA; DNA
 A;Residues: 1-614 <SOR>
 A;Cross-references: UNIPROT:P22303; GB:M55040; NID:g177974; PIDN:AAA68151.1; PID:g177975
 A;Note: this sequence represents a composite of clones including clone ABGACHE from adult
 ne should represent an authentic brain splice form
 R;Chhajlani, V.; Derr, D.; Earles, B.; Schmeil, E.; August, T.
 FEBS Lett. 247, 279-282, 1989
 A;Title: Purification and partial amino acid sequence analysis of human erythrocyte acet
 A;Reference number: S03959; MUID:89232136; PMID:2714437
 A;Accession: S03959
 A;Molecule type: protein
 A;Residues: 256-266, 'Y', 268-273, 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-326;
 Y, 532-551 <CHH>
 A;Experimental source: erythrocytes
 A;Note: this form was a disulfide-linked homodimer
 C;Genetics:

A;Gene: GDB:ACHE; YT
 A;Cross-references: GDB:118746; OMIM:100740
 A;Map position: 7q22-7q22
 C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidyl
 F;63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
 |||||
 Db 586 AEFHRWSSVMVHWK 599

RESULT 4

JH0314
 acetylcholinesterase (EC 3.1.1.7) precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
 C;Accession: JH0314
 R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
 Neuron 5, 317-327, 1990
 A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
 A;Reference number: JH0314; MUID:90380429; PMID:2400605
 A;Accession: JH0314
 A;Molecule type: mRNA
 A;Residues: 1-614 <RAC>
 A;Cross-references: UNIPROT:P21836; EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845
 A;Experimental source: brain
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-614/Product: acetylcholinesterase #status predicted <MAT>
 F;63-569/Domain: cholinesterase homology <CHE>
 F;100-127,288-303,440-560/Disulfide bonds: #status predicted
 F;234/Active site: Ser #status predicted
 F;296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
 |||||
 Db 586 AEFHRWSSVMVHWK 599

RESULT 5

JH0811
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Accession: JH0811
 R;Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.
 J. Neurochem. 60, 337-346, 1993
 A;Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul
 A;Reference number: JH0811; MUID:93107932; PMID:8417155
 A;Accession: JH0811
 A;Molecule type: mRNA
 A;Residues: 1-614 <LEG>
 A;Cross-references: UNIPROT:P37136; GB:S50879; NID:g262092; PIDN:AAB24586.1; PID:g262093

A;Experimental source: striatum
 C;Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
 F;63-569/Domain: cholinesterase homology <CHE>
 F;100-127,288-303,440-560/Disulfide bonds: #status predicted
 F;234,365,478/Active site: Ser, Glu, His #status predicted
 F;296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMHVK 14
 |||||
 Db 586 AEFHRWSSYMHVK 599
 |||||
 RESULT 6
 ACRYE
 acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric ray
 N:Alternate names: acetylcholinesterase, asymmetric form
 C:Species: Torpedo californica (Pacific electric ray)
 C:Date: 17-Mar-1987 #sequence_revision 08-Nov-1986 #text_change 09-Jul-2004
 C:Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
 R:Schumacher, M.; Camp, S.; Maullet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; Fed. Proc. 45, 2976-2981, 1986
 Nature 319, 407-409, 1986
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its
 A:Reference number: A00773; MUID:86118676; PMID:3753747
 A:Accession: A00773
 A:Molecule type: mRNA
 A:Residues: 'NS', 11-596 <SCH>
 A:Cross-references: UNIPROT:P04058; GB:X03439; NID:G64389
 A:Experimental source: electric organ
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature protein
 R:Schumacher, M.; Camp, S.; Maullet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; Fed. Proc. 45, 2976-2981, 1986
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and function
 A:Reference number: A60820; MUID:87054662; PMID:3536598
 A:Accession: A60820
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 22-596 <SC2>
 R:Schumacher, M.; Maullet, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase
 A:Reference number: A32701; MUID:89066695; PMID:3198606
 A:Accession: A31962
 A:Molecule type: mRNA
 A:Residues: 1-23 <SC3>
 A:Cross-references: EMBL:X03439; NID:G64389
 A:Experimental source: clones AChE-11 and AChE-18
 A:Note: revision to sequence A00773
 A:Accession: B31962
 A:Molecule type: DNA; mRNA
 A:Residues: 499-565 <SC4>
 A:Cross-references: GB:X03439; NID:G64389
 A:Experimental source: clone AChE-1
 R:MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase
 A:Reference number: A23902; MUID:86008285; PMID:3900071
 A:Accession: A23902
 A:Molecule type: protein
 A:Residues: 22, 'B', 24-45, 214-237 <MAC>
 A:Note: active site Ser identification
 R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A:Title: Anionic subunits of the catalytic center of acetylcholinesterase from Torpedo a
 A:Reference number: A41117; MUID:91296772; PMID:2068091
 A:Accession: B41117
 A:Molecule type: protein
 A:Residues: 100-108 <KRE>
 A:Note: substrate binding site
 R:Maullet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A:Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinester
 A:Reference number: P50113; MUID:90166618; PMID:2306366
 A:Accession: S15677
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 557-596 <NAU>
 A:Cross-references: EMBL:X56516
 R:MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986

A:Title: Profile of the disulfide bonds in acetylcholinesterase.
 A:Reference number: A43099; MUID:87008586; PMID:3759980
 A:Contents: annotation; disulfide bonds
 R:Sussman, J.L.; Harel, M.; Silman, I.
 submitted to the Brookhaven Protein Data Bank, October 1991
 A:Reference number: A50061; PDB:1ACE
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of
 R:Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Toker, L.; Silman, I.
 Science 253, 872-879, 1991
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic
 A:Reference number: A43098; MUID:91343928; PMID:1678899
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of
 C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a
 cholinesterase occurs on the outer surfaces of cell membranes, including those of erythro
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of
 C:Function:
 A:Description: hydrolyzes acetylcholine to choline and acetate
 A:Pathway: neurotransmitter degradation
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane pro
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
 F:51-551/Domain: cholinesterase homology <CHE>
 F:80-478, 554/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:188-115, 275-286, 423-542/Disulfide bonds: #status experimental
 F:105/Binding site: substrate (Trp) #status experimental
 F:221/Active site: Ser #status experimental
 F:348, 461/Active site: Glu, His #status predicted
 F:437/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:593/Disulfide bonds: interchain #status experimental
 Query Match 92.0%; Score 80; DB 1; Length 596;
 Best Local Similarity 92.3%; Pred. No. 0.00011;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EFRHSSYMHVK 14
 |||||
 Db 569 EFRHSSYMHVK 581
 |||||
 RESULT 7
 A38868
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
 C:Species: Torpedo marmorata (marbled electric ray)
 C:Date: 23-Apr-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: A38868; A29682; S15696; A25650
 R:Massoulie, J.; Bon, S.
 submitted to the EMBL Data Library, June 1992
 A:Reference number: A38868
 A:Accession: A38868
 A:Molecule type: mRNA
 A:Residues: 1-599 <MAS>
 A:Cross-references: UNIPROT:P07692; EMBL:X05497; NID:G64414; PIDN:CAA29047.1; PID:G64415
 R:Sikorav, J.L.; Krejci, E.; Massoulie, J.
 EMBO J. 6, 1865-1873, 1987
 A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of
 A:Reference number: A29682; MUID:88004392; PMID:2820709
 A:Accession: A29682
 A:Molecule type: mRNA
 A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>
 A:Cross-references: EMBL:X05497
 R:Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;
 EMBO J. 7, 2983-2993, 1988
 A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo ele
 A:Reference number: S01293; MUID:89030590; PMID:3181125
 A:Accession: S15696
 A:Molecule type: mRNA
 A:Residues: 526-599 <SI2>
 A:Cross-references: EMBL:X13172; NID:G64416; PIDN:CAA31570.1; PID:G64417
 A:Experimental source: clone pAChE2
 R:Bon, S.; Chang, J.Y.; Strosberg, A.D.
 FEBS Lett. 209, 206-212, 1986
 A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu

inesterase.

A;Reference number: A91370; MUID:87080761; PMID:3792544
 A;Accession: A25650
 A;Molecule type: protein
 A;Residues: 25-40,'G',42-47 <BON>
 C;Genetics:
 A;Gene: AChE
 C;Function:
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmission
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-59/Product: acetylcholinesterase #status predicted <MAT>
 F;54-55/Domain: cholinesterase homology <CHE>
 F;83,440,481,557/Binding site: carbohydrtate (Asn) (covalent) #status predicted
 F;91-118,278-289,426-545/Disulfide bonds: #status predicted
 F;224,351,464/Active site: Ser, Glu, His #status predicted
 F;596/Disulfide bonds: interchain #status predicted

Query Match 92.0%; Score 80; DB 1; Length 599;
 Best Local Similarity 92.3%; Pred. No. 0.00011;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFHRWSSVMVHWK 14
 |||||:||||:||||
 Db 572 EFHRWSSVMVHWK 584

RESULT 8

acetylcholinesterase (EC 3.1.1.7) - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 A;Accession: S47639
 R;Randall, W.R.; Rimer, M.; Gough, N.R.
 Biochim. Biophys. Acta 1218, 453-456, 1994
 A;Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and brain
 A;Reference number: S47639; MUID:94325359; PMID:8049273
 A;Accession: S47639
 A;Molecule type: mRNA
 A;Residues: 1-767 <RAN>
 A;Cross-references: UNIPROT:P36196; EMBL:U03472; NID:G623031; PIDN:AAA60456.1; PID:94241
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: carboxylic ester hydrolase

Query Match 74.7%; Score 65; DB 2; Length 767;
 Best Local Similarity 76.9%; Pred. No. 0.027;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EFHRWSSVMVHWK 14
 |||||:||||:||||
 Db 740 EFHRWSSVMVGRW 752

RESULT 9

cholinesterase (EC 3.1.1.8) precursor [validated] - human
 N;Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C;Accession: A33769; A26613; A33887; A34668; A00772
 R;Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
 Biochemistry 29, 124-131, 1990
 A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single copy
 A;Reference number: A33769; MUID:90212557; PMID:2322535
 A;Accession: A33769
 A;Molecule type: DNA
 A;Residues: 'MSVQNLQAGAAASCIPKYMIPTCKLHLCRESEIN',1-602 <ARP>
 A;Cross-references: UNIPROT:P06276; GB:M32391; GB:J02879
 A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation
 R;Prody, C.A.; Zevin-Sonkin, D.; Gnat, A.; Goldberg, O.; Soreq, H.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987

A;Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase

A;Reference number: A26613; MUID:87231856; PMID:3035536

A;Accession: A26613

A;Molecule type: mRNA

A;Residues: 1-133,'D',135-602 <PRO>

R;McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose,

Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987

A;Title: Brain cDNA clone for human cholinesterase.

A;Reference number: A33887; MUID:88016155; PMID:3477799

A;Accession: A33887

A;Molecule type: mRNA

A;Residues: 'MSVQNLQAGAAASCIPKYMIPTCKLHLCRESEIN',1-602 <MCT>

A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation

R;Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,

Am. J. Hum. Genet. 46, 934-942, 1990

A;Title: Identification of a frameshift mutation responsible for the silent phenotype of

A;Reference number: A34668; MUID:90252779; PMID:2339692

A;Accession: A34668

A;Molecule type: DNA

A;Residues: 143-145,'VSNWNIPTCL' <NOG>

A;Note: frameshift mutant in codon for residue 145 (Gly)

R;Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.

J. Biol. Chem. 262, 549-557, 1987

A;Title: Complete amino acid sequence of human serum cholinesterase.

A;Reference number: A00772; MUID:87109144; PMID:3542989

A;Accession: A00772

A;Molecule type: protein

A;Residues: 29-602 <LOC>

A;Experimental source: plasma

C;Comment: Cholinesterase is present in most cells (except erythrocytes).

C;Genetics:

A;Gene: GDB:BCHE; CHE1

A;Cross-references: GDB:120558; OMIM:177400

A;Map position: 3q26.1-3q26.2

A;Introns: 506/2; 562/1

C;Function:

A;Description: hydrolyzes acylcholines to choline and a carboxylic acid

A;Note: this cholinesterase is highly reactive with organophosphate esters

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer

F;1-28/Domain: signal sequence #status predicted <SIG>

F;29-602/Product: cholinesterase #status experimental <MAT>

F;56-556/Domain: cholinesterase homology <CHE>

F;45,85,134,269,284,369,483,509,514/Binding site: carbohydrtate (Asn) (covalent) #status

F;226/Active site: Ser #status experimental

Query Match 71.3%; Score 62; DB 1; Length 602;
 Best Local Similarity 64.3%; Pred. No. 0.061;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
 |||||:||||:||||
 Db 573 AGFHRWNNYMDWK 586

RESULT 10

cholinesterase (EC 3.1.1.8) - rabbit
 N;Alternate names: butyrylcholinesterase
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S10255; C39768
 R;Jbilo, O.; Chatonnet, A.
 Nucleic Acids Res. 18, 3990, 1990
 A;Title: Complete sequence of rabbit butyrylcholinesterase.
 A;Reference number: S10255; MUID:90326526; PMID:2374720
 A;Accession: S10255
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-581 <JBI>
 A;Cross-references: UNIPROT:P21927; EMBL:X52090; NID:q1476; PIDN:CAA36308.1; PID:q137027
 R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
 J. Biol. Chem. 266, 6966-6974, 1991

A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: C39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 75-215 <ARP>
A;Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789
C;Genetics:
A;Introns: 485/2; 541/1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F:35-535/Domain: cholinesterase homology <CHE>

Query Match 70.1%; Score 61; DB 2; Length 581;
Best Local Similarity 64.3%; Pred. No. 0.084;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | : | |
Db 552 AGFHRWNNYMAWK 565

RESULT 11
S70849
cholinesterase (EC 3.1.1.8) - mouse
N;Alternate names: butyrylcholine esterase
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S70849; S15680; A39768
R;Taylor, P.
submitted to the EMBL Data Library, August 1992
A;Reference number: S70849
A;Accession: S70849
A;Molecule type: nucleic acid
A;Residues: 1-603 <TAY>
A;Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:g191579; PIDN:AAA37328.1; PID:g191579
R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternative splicing
A;Reference number: JH0314; MUID:90380429; PMID:2400605
A;Accession: S15680
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 30-128,'P',130-603 <RAC>
A;Cross-references: EMBL:M99492
R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogaj, M.
J. Biol. Chem. 266, 6366-6374, 1991
A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: A39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 97-128,'P',130-237 <ARP>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F:57-557/Domain: cholinesterase homology <CHE>

Query Match 70.1%; Score 61; DB 2; Length 603;
Best Local Similarity 64.3%; Pred. No. 0.088;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | : | |
Db 574 AGFHRWNNYMDWQ 587

RESULT 12
T12393
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Arabidopsis thaliana chloroplast
C;Species: chloroplast Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12393
R;Galloway, G.L.; Malmberg, R.L.; Price, R.A.

Mol. Biol. Evol. 15, 1312-1320, 1998
A;Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example from Arabidopsis
A;Reference number: Z16357; MUID:99003705; PMID:9787437
A;Accession: T12393
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-260 <GAL>
A;Cross-references: UNIPROT:O78318; EMBL:AF064654; NID:g3366917; PID:g3366918; PIDN:AAAC6918
C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 50.6%; Score 44; DB 2; Length 260;
Best Local Similarity 41.7%; Pred. No. 16;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 FHRWSSYVHWK 14
| | | | | : | : | |
Db 192 FQKNSKRIHWE 203

RESULT 13
D86339
protein F2D10.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86339
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafci, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, B.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 <STO>
A;Cross-references: UNIPROT:Q9LM89; GB:AE005172; NID:g8886950; PIDN:AAF80636.1; GSPDB:GN0636.1
C;Genetics:
A;Gene: F2D10.14
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g23160

Query Match 49.4%; Score 43; DB 2; Length 422;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 9; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 AEFHRWSSYVHWK 14
| | | | | : | : | |
Db 328 AEKQWSSYIVLPPPWK 345

RESULT 14
S67037
SMP3 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O3527; protein YOR149c
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67037; S13750
R;Bordonne, R.; Camases, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winsor, B.J.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67032
A;Accession: S67037
A;Molecule type: DNA
A;Residues: 1-516 <BOR>
A;Cross-references: UNIPROT:Q04174; EMBL:Z75057; NID:g1420374; PID:e252038; PID:g1420375

A;Experimental source: strain S288C
R;Irie, K.; Araki, H.; Oshima, Y.
Mol. Gen. Genet. 225, 257-265, 1991
A;Title: Mutations in a Saccharomyces cerevisiae host showing increased holding stability
A;Reference number: S13750; UID:91172125; PMID:2005867
A;Accession: S13750
A;Molecule type: DNA
A;Residues: 1-121, 'IK', 124-162, 'G', 164-168, 'R', 170-278, 'L', 280-516 <IRI>
A;Cross-references: EMBL:X58121; NID:94497; PIDN:CAA41123.1; PID:94498
C;Genetics:
A;Gene: SGD:SMP3
A;Cross-references: SGD:S0005675; MIPS:YOR149C
A;Map position: 13R
F;9-25/Domain: transmembrane #status predicted <TM1>
F;189-205/Domain: transmembrane #status predicted <TM2>
F;215-231/Domain: transmembrane #status predicted <TM3>
F;271-287/Domain: transmembrane #status predicted <TM4>
F;344-360/Domain: transmembrane #status predicted <TM5>
Query Match 49.4%; Score 43; DB 2; Length 516;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 6 WSSYVWVHWK 14
Db 204 WKFYRVHWK 212
RESULT 15
A87273
conserved hypothetical protein CC0194 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87273
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; UID:21173698; PMID:11259647
A;Accession: A87273
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <STO>
A;Cross-references: UNIPROT:Q9ABN2; GB:AE005673; NID:gl3421317; PIDN:AAK22181.1; GSPDB:G
C;Genetics:
A;Gene: CC0194
Query Match 48.3%; Score 42; DB 2; Length 100;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 EFHRWSSYVWVHWK 14
Db 64 EFHRASPHMAAWR 76
RESULT 16
T08878
supervillin P205 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08878
R;Pestonjans, K.N.; Pope, R.K.; Wulfschle, J.D.; Luna, E.J.
J. Cell Biol. 139, 1255-1269, 1997
A;Title: Supervillin (P205): A novel membrane associated membrane associated F-actin bin
A;Reference number: 216509; UID:98044228; PMID:9382871
A;Accession: T08878
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1792 <PES>
A;Cross-references: UNIPROT:O46385; EMBL:AF025996; NID:g2668622; PIDN:AAC48783.1; PID:g2

A;Experimental source: cell line MDBK (Madin Darby Bovine Kidney); ATCC CCL-22
C;Keywords: actin binding; cell adhesion; membrane-associated protein
F;1732-1792/Domain: villin headpiece homology <VHH>
Query Match 48.3%; Score 42; DB 2; Length 1792;
Best Local Similarity 46.2%; Pred. No. 2e+02; 4; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 EFHRWSSYVWVHWK 14
Db 1352 QFHEGDYVWVWVK 1364
RESULT 17
C96911
transcription regulators, LysR family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C96911
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo.
A;Reference number: A96900; UID:21359325; PMID:21359325
A;Accession: C96911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: UNIPROT:Q97MU8; GB:AE001437; PIDN:AAK78078.1; PID:gl5022917; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0093
Query Match 47.1%; Score 41; DB 2; Length 290;
Best Local Similarity 54.5%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 EFHRWSSYVWVHWK 12
Db 262 EYHRYFSYLCH 272
RESULT 18
A75137
hypothetical protein PAB0600 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75137
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KAW>
A;Cross-references: UNIPROT:Q9V095; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB4981
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0600
Query Match 47.1%; Score 41; DB 2; Length 397;
Best Local Similarity 40.0%; Pred. No. 68;
Matches 6; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
Qy 2 EFH--RWSSYVWVHWK 14
Db 18 DYHVKRWKQKLHWK 32
RESULT 19
F96741
probable sucrose transport protein F17M19.4 [imported] - Arabidopsis thaliana

```
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96741
R;Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96741
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
A;Cross-references: UNIPROT:Q9C8X2; GB:AE005173; NID:G6978914; PIDN:AAF34306.1; GSPDB:GN
C;Genetics:
A;Gene: F17M19.4
A;Map position: 1
C;Superfamily: common tobacco sucrose transport protein

Query Match 47.1%; Score 41; DB 2; Length 512;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HRWSSYM 10
Db 66 HRWSSYM 72

RESULT 20
A97177
site-specific recombinase, DNA invertase Pin homolog [imported] - Clostridium acetobutyli
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97177
R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97177
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-523 <KUR>
A;Cross-references: UNIPROT:Q97GW8; GB:AE001437; PIDN:AAK80204.1; PID:G15025248; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2247

Query Match 47.1%; Score 41; DB 2; Length 523;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HRWSSYMVH 12
Db 231 HRWQYMIN 239

RESULT 21
B83936
hypothetical protein BH2290 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B83936
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83936
```

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <STO>
A;Cross-references: UNIPROT:Q9KAJ7; GB:AP001515; GB:BA000004; NID:G10174886; PIDN:BA8060
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2290

Query Match 47.1%; Score 41; DB 2; Length 535;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EFHRWSSYMV 11
Db 172 KFHRWFSLMV 181

RESULT 22
H83904
hypothetical protein BH2040 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83904
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83904
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-818 <STO>
A;Cross-references: UNIPROT:Q9KB88; GB:AP001514; GB:BA000004; NID:G10174613; PIDN:BA8057
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2040

Query Match 47.1%; Score 41; DB 2; Length 818;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HRWSSYMVHWK 14
Db 369 NEWSHLITWK 379

RESULT 23
T30253
spalt protein - mouse (fragment)
N;Alternate names: zinc finger protein msal
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30253
R;Ott, T.; Kaestner, K.H.; Monaghan, A.P.; Schutz, G.
Mech. Dev. 56, 117-128, 1996
A;Title: The mouse homolog of the region specific homeotic gene spalt of Drosophila is e
A;Reference number: Z20791; MUID:96391179; PMID:8798152
A;Accession: T30253
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1323 <OTT>
A;Cross-references: UNIPROT:Q62255; EMBL:X97581; NID:G1296844; PIDN:CAA66196.1; PID:G129
C;Genetics:
A;Gene: msal
C;Function:
A;Description: may play an important role in the development of the nervous system

Query Match 47.1%; Score 41; DB 2; Length 1323;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
Db 29 AEFKWADFLQHK 42
```

RESULT 24

S64059

stearoyl-CoA 9-desaturase (EC 1.14.19.1) - yeast (Saccharomyces cerevisiae)

N;Alternate names: Delta9 fatty acid desaturase; protein G3472; protein YGL055w

C;Species: Saccharomyces cerevisiae

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C;Accession: S64059; A23675

R;Feuermann, M.; Potier, S.; Souciet, J.L.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64044

A;Accession: S64059

A;Molecule type: DNA

A;Residues: 1-510 <FEU>

A;Cross-references: UNIPROT:P21147; EMBL:Z72577; NID:g1322551; PIDN:CAA96757.1; PID:g1322551

A;Experimental source: strain S288C

R;Strukey, J.E.; McDonough, V.M.; Martin, C.E.

J. Biol. Chem. 265, 20144-20149, 1990

A;Title: The OLE1 gene of Saccharomyces cerevisiae encodes the delta9 fatty acid desaturase

A;Reference number: A23675; MUID:91056050; PMID:1978720

A;Accession: A23675

A;Molecule type: DNA

A;Residues: 1-303, 'M', 305-510 <STU>

A;Cross-references: GB:J05676; NID:g172063; PIDN:AAA34826.1; PID:g172064

C;Genetics:

A;Gene: SGD:OLE1; MDM2; MIPS:YGL055w

A;Cross-references: SGD:S0003023; MIPS:YGL055w

A;Map position: 7L

C;Superfamily: Delta-9 acyl-CoA desaturase with heme/steroid binding domain; cytochrome

C;Keywords: endoplasmic reticulum; heme; iron; metalloprotein; oxidoreductase; transmembrane

F;116-132/Domain: transmembrane #status predicted <TM1>

F;141-157/Domain: transmembrane #status predicted <TM2>

F;155-345/Domain: stearyl-CoA desaturase homology <SDH>

F;257-273/Domain: transmembrane #status predicted <TM3>

F;409-486/Domain: cytochrome b5 core homology <CB5>

F;444,470/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 46.6%; Score 40.5; DB 1; Length 510;

Best Local Similarity 56.2%; Pred. No. 1e+02;

Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 2;

Qy 1 AEFHR-WS--SYMVHW 13

| | | | | | | |

Db 158 AGYHRLWSRSYSAHW 173

RESULT 25

PH1152

IG heavy chain V region (clone 47F.2A) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: PH1152

R;Schitteck, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A;Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A;Reference number: PH1105; MUID:92364545; PMID:1500855

A;Accession: PH1152

A;Molecule type: DNA

A;Residues: 1-90 <SCH>

A;Cross-references: UNIPROT:Q91VA2; UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924P7; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q924Q5

A;Experimental source: B cell

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 46.0%; Score 40; DB 2; Length 90;

Best Local Similarity 46.2%; Pred. No. 23;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AEFHRSSYMVHW 13

| | | | | | | |

```
A;Cross-references: UNIPROT:P53237; EMBL:Z72842; NID:gl1323070; PID:gl1323071; GSPDB:GN000
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:LST7; MIPS:YGR057c
A;Cross-references: SGD:S0003289
A;Map position: 7R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YGR057c

Query Match 46.0%; Score 40; DB 2; Length 245;
Best Local Similarity 44.4%; Pred. No. 61;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HRWSSYMYVH 12
|:|:|:|
Db 228 HKNSFLH 236

RESULT 29
A64546
hypothetical protein HP0209 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64546
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64546
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-450 <TOM>
A;Cross-references: UNIPROT:O25000; GB:AE000541; GB:AE000511; NID:g2313299; PIDN:AAD0728
C;Genetics:
A;Start codon: GTG
C;Superfamily: Helicobacter pylori hypothetical protein HP0209

Query Match 46.0%; Score 40; DB 2; Length 450;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FHRWSSYMYVHW 13
|:|:|:|
Db 179 FYRWKKFRIEW 189

RESULT 30
T30341
zinc finger protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30341
R;Holleman, T.; Schuh, R.; Pieler, T.; Stick, R.
Mech. Dev. 55, 19-32, 1996
A;Title: Xenopus Xsai-1, a vertebrate homolog of the region specific homeotic gene spalt
A;Reference number: Z20832; MUID:96317243; PMID:8734496
A;Accession: T30341
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1350 <HOL>
A;Cross-references: UNIPROT:Q91929; EMBL:L46583; NID:gl235930; PID:gl235931; PIDN:AAC422
C;Genetics:
A;Note: Xsai-1

Query Match 46.0%; Score 40; DB 2; Length 1350;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMYVHWK 14
|:|:|:|:|
Db 70 AEFKWTDFLDHKK 83
```

```
RESULT 31
T08166
probable membrane protein 1995 - Chlamydomonas reinhardtii chloroplast
C;Species: chloroplast Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08166; A24829
R;Boudreau, E.; Turmel, M.; Goldschmidt-Clermont, M.; Rochaix, J.D.; Sivan, S.; Michaels
Mol. Gen. Genet. 253, 649-653, 1997
A;Title: A large unidentified open reading frame (ORF1995) in Chlamydomonas reinhardtii
A;Reference number: Z16392; MUID:97218038; PMID:9065699
A;Accession: T08166
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1995 <BOU>
A;Cross-references: UNIPROT:P36495; EMBL:X92726; NID:gl054719; PIDN:CAA63385.1; PID:gl05
R;Woessner, J.P.; Gillham, N.W.; Boynton, J.E.
Gene 44, 17-28, 1986
A;Title: The sequence of the chloroplast atpB gene and its flanking regions in Chlamydom
A;Reference number: A24829; MUID:87031585; PMID:2876928
A;Accession: A24829
A;Molecule type: DNA
A;Residues: 1925-1995 <WOE>
A;Cross-references: GB:M13704; NID:g336666; PIDN:AAA84144.1; PID:g895614
A;Note: the authors translated the codon GAA for residue 1957 as Gly
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast; membrane protein

Query Match 46.0%; Score 40; DB 2; Length 1995;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RWSSYMYVHWK 14
|:|:|:|:|
Db 882 RWTYMQHYK 891

RESULT 32
S74825
probable Rieske iron-sulfur protein slr1747 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74825
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74825
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-469 <KAN>
A;Cross-references: UNIPROT:P73738; EMBL:D90909; GB:AB001339; NID:gl652844; PIDN:BAAL778
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Nostoc sp. cell death suppressor protein; Rieske [2Fe-2S] homology
C;Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F;66-114/Domain: Rieske [2Fe-2S] homology <RSK>
F;76,78,96,99/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status predi

Query Match 45.4%; Score 39.5; DB 2; Length 469;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AEFHRW-SSYMYV 11
|:|:|:|:|
Db 349 AEFHRWIEQYQV 360

RESULT 33
```


T02379
 Hypothetical protein At2g44230 [imported] - Arabidopsis thaliana
 N;Alternate names: hypothetical protein F411.4
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C;Accession: T02379; A84876
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, May 1998
 A;Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
 A;Reference number: Z14667
 A;Accession: T02379
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-542 <ROU>
 A;Cross-references: UNIPROT:O64858; EMBL:AC004521; NID:G3128166; PID:G3128170
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: A84876
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-542 <STO>
 A;Cross-references: GB:AE002093; NID:G3128170; PIDN:AAIC16074.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g44230; F411.4
 A;Map position: 2
 A;Introns: 32/1

Query Match 45.4%; Score 39.5; DB 2; Length 542;
 Best Local Similarity 40.0%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

Qy 1 AEFHR-----WSSYVHW 13
 ||| : : : : :
 Db 464 AEFMRGELEPWLNYMRHW 483

RESULT 34
 T09856
 sucrose synthase (EC 2.4.1.13) - upland cotton (fragment)
 C;Species: Gossypium hirsutum (upland cotton)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T09856
 R;Shimizu, Y.; Aotsuka, S.; Hasegawa, O.; Kawada, T.; Sakuno, T.; Sakai, F.; Hayashi, T.
 Plant Cell Physiol. 38, 375-378, 1997
 A;Title: Changes in levels of mRNAs for cell wall-related enzymes in growing cotton fibre
 A;Reference number: Z16889; MUID:97294938; PMID:9150611
 A;Accession: T09856
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-100 <SHI>
 A;Cross-references: UNIPROT:O23949; EMBL:D88412; NID:G2244729; PIDN:BAA21106.1; PID:G224
 A;Experimental source: strain Coker312; fiber
 C;Function:
 A;Description: catalyzes reversible cleavage of sucrose into UDP-glucose and D-fructose
 C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
 C;Keywords: Glycosyltransferase; hexosyltransferase

Query Match 44.8%; Score 39; DB 2; Length 100;
 Best Local Similarity 35.7%; Pred. No. 37;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 ||| : : : : :
 Db 80 ASFPKXNRLIHWQ 93

RESULT 35
 HVMST7

Ig heavy chain precursor V region (TEPC 1017) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
 C;Accession: A02033
 R;Gilliam, A.C.; Shen, A.; Richards, J.E.; Blattner, F.R.; Mushinski, J.F.; Tucker, P.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4164-4168, 1984
 A;Title: Illegitimate recombination generates a Class switch from C-mu to C-delta in an
 A;Reference number: A02033; MUID:84248078; PMID:6429663
 A;Accession: A02033
 A;Molecule type: mRNA
 A;Residues: 1-138 <GIL>
 A;Cross-references: UNIPROT:P03980
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-117/Region: V segment
 F;34-117/Domain: immunoglobulin homology <IMV>
 F;118-123/Region: D segment
 F;124-138/Region: J segment
 Query Match 44.8%; Score 39; DB 1; Length 138;
 Best Local Similarity 38.5%; Pred. No. 50;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHW 13
 ||| : : : : :
 Db 43 ASGHTFTNYIHW 55

RESULT 36
 B82315
 hypothetical protein VC0496 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: B82315
 R;Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, P.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: B82315
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-199 <HEI>
 A;Cross-references: UNIPROT:Q9KUL9; GB:AE004136; GB:AE003852; NID:G9654921; PIDN:AAF9366
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC0496
 A;Map position: 1
 C;Superfamily: yagK protein

Query Match 44.8%; Score 39; DB 2; Length 199;
 Best Local Similarity 58.3%; Pred. No. 71;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FHRWSSYVHWK 14
 ||| : : : : :
 Db 177 FHRLSFAEAWK 188

RESULT 37
 S37434
 membrane glycoprotein - porcine epidemic diarrhea virus
 C;Species: porcine epidemic diarrhea virus
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S37434
 R;Duarte, M.
 submitted to the EMBL Data Library, July 1993
 A;Reference number: S37432
 A;Accession: S37434
 A;Status: preliminary

A:Molecule type: genomic RNA
A:Residues: 1-226 <DUA>
A:Cross-references: UNIPROT:P59771; UNIPROT:P59770; EMBL:Z24733; NID:g406754; PIDN:CAA80
C:Superfamily: coronavirus E1 membrane glycoprotein

Query Match 44.8%; Score 39; DB 2; Length 226;
Best Local Similarity 45.5%; Pred. No. 80;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 FHRWSSVMVHW 13
|:|:|:|:|
Db 65 FDWASFOVNW 75

RESULT 38
D49591
membrane protein M - porcine epidemic diarrhea virus
C:Species: porcine epidemic diarrhea virus
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
A:Accession: D49591
R:Duarte, M.; Tobler, K.; Bridgen, A.; Raschaert, D.; Ackermann, M.; Laude, H.
Virology 198, 466-476, 1994
A:Title: Sequence analysis of the porcine epidemic diarrhea virus genome between the nuc
A:Reference number: A49591; MUID:94120721; PMID:8291230
A:Accession: D49591
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-226 <DUA>
A:Cross-references: UNIPROT:Q91AU9; GB:Z24733
C:Superfamily: coronavirus E1 membrane glycoprotein

Query Match 44.8%; Score 39; DB 2; Length 226;
Best Local Similarity 45.5%; Pred. No. 80;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 FHRWSSVMVHW 13
|:|:|:|:|
Db 65 FDWASFOVNW 75

RESULT 39
T12386
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Sisymbrium altissimum chloropl
C:Species: chloroplast Sisymbrium altissimum
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
A:Accession: T12386
R:Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A:Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fr
A:Reference number: Z16357; MUID:99003705; PMID:9787437
A:Accession: T12386
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-259 <GAL>
A:Cross-references: UNIPROT:O78312; EMBL:AF064648; NID:g3366905; PID:g3366906; PIDN:AAC6
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 44.8%; Score 39; DB 2; Length 259;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 FHRWSSVMVHW 14
|:|:|:|:|
Db 192 FQKWSKRIRWE 203

RESULT 40
T12395
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Thlaspi arvense chloroplast (fra

C:Species: chloroplast Thlaspi arvense
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
A:Accession: T12395
R:Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A:Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fr
A:Reference number: Z16357; MUID:99003705; PMID:9787437
A:Accession: T12395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-260 <GAL>
A:Cross-references: UNIPROT:O78320; EMBL:AF064656; NID:g3366921; PID:g3366922; PIDN:AAC6
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 44.8%; Score 39; DB 2; Length 260;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 FHRWSSVMVHW 14
|:|:|:|:|
Db 192 FQKWSKRIRWE 203

RESULT 41
T12394
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Stanleya pinnata chloroplast (fr
C:Species: chloroplast Stanleya pinnata
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
A:Accession: T12394
R:Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A:Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fr
A:Reference number: Z16357; MUID:99003705; PMID:9787437
A:Accession: T12394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-260 <GAL>
A:Cross-references: UNIPROT:O78319; EMBL:AF064655; NID:g3366919; PID:g3366920; PIDN:AAC6
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 44.8%; Score 39; DB 2; Length 260;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 FHRWSSVMVHW 14
|:|:|:|:|
Db 192 FQKWSKRIRWE 203

RESULT 42
T14435
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - wild cabbage chloroplast (fragme
C:Species: chloroplast Brassica oleracea (wild cabbage)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A:Accession: T14435
R:Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A:Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fr
A:Reference number: Z16357; MUID:99003705; PMID:9787437
A:Accession: T14435
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-260 <GAL>
A:Cross-references: UNIPROT:O78311; EMBL:AF064647; NID:g3366903; PIDN:AAC68586.1; PID:g3
C:Genetics:

```
A;Gene: ndhF
A;Genome: chloroplast
A;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match      44.8%; Score 39; DB 2; Length 260;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FHRWSSYVHWK 14
   | : | | | : | :
Db 192 FQKWSKRIRWE 203

RESULT 43
F89904
glycerol uptake facilitator [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89904
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89904
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <KUR>
A;Cross-references: UNIPROT:Q99UH4; GB:BA000018; PID:g13701099; PIDN:BA042394.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: glpF

Query Match      44.8%; Score 39; DB 2; Length 272;
Best Local Similarity 55.6%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 WSSYVHWK 14
   | : | | |
Db 101 WLMYLPHWK 109

RESULT 44
D83191
conserved hypothetical protein PA3631 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83191
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83191
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:Q9HXZ9; GB:AE004783; GB:AE004091; NID:g9949786; PIDN:AAG0701
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3631
C;Superfamily: Campylobacter jejuni probable integral membrane protein Cj1500

Query Match      44.8%; Score 39; DB 2; Length 408;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EFHRWSSYVHWK 13
   | : | | | : | :
Db 45 EFTRWGGHVLGW 56
```

RESULT 45

```
B42249
serine-type carboxypeptidase (EC 3.4.16.-) sxa2 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: B42249; T37564
R;Imai, Y.; Yamamoto, M.
Mol. Cell. Biol. 12, 1827-1834, 1992
A;Title: Schizosaccharomyces pombe sxa1(+) and sxa2(+) encode putative proteases involve
A;Reference number: A42249; MUID:92195329; PMID:1549128
A;Accession: B42249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-507 <IMA>
A;Cross-references: UNIPROT:P32825; GB:D10199; NID:g218559; PIDN:BAA01047.1; PID:g218560
R;Wood, V.; Barrall, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21725
A;Accession: T37564
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-507 <WOO>
A;Cross-references: EMBL:AL035439; PIDN:CAB36509.1; GSPDB:GN000066; SPDB:SPAC1296.03c
A;Experimental source: strain 972h-; cosmid c1296
C;Genetics:
A;Gene: sxa2
A;Map position: 1
C;Superfamily: Serine carboxypeptidase
C;Keywords: hydrolase; serine carboxypeptidase

Query Match      44.8%; Score 39; DB 2; Length 507;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 HRWSSYVHWK 14
   | : | | |
Db 21 HALFTYVHWK 31
```

Search completed: October 12, 2005, 10:20:09
Job time : 27 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:06:29 ; Search time 165 Seconds
(without alignments)
32.816 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRWSSYNVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	14	2	AAW35340 Human ace
2	87	100.0	14	4	AAU04701 Scrambled
3	87	100.0	14	5	ABG65979 Human ace
4	87	100.0	39	2	AAW77010 Alternati
5	87	100.0	40	4	AB48915 Human ace
6	87	100.0	40	4	AB50033 Acetylcho
7	87	100.0	40	5	AAU98023 Human syn
8	87	100.0	44	4	AAU04705 Rat acety
9	87	100.0	44	4	AAU04704 Mouse ace
10	87	100.0	44	4	AAU04702 Human ace
11	87	100.0	44	4	ABG65951 Mouse ace
12	87	100.0	44	4	ABG65949 Human ace
13	87	100.0	44	4	ABG65952 Rat acety
14	87	100.0	45	2	AAW74586 Amino aci
15	87	100.0	45	2	AAW48800 C-termina
16	87	100.0	45	2	AAW68144 Human ACh
17	87	100.0	53	4	AAU04299 Bovine ac
18	87	100.0	53	4	ABG65953 Bovine ac
19	87	100.0	54	4	AAU04703 Rabbit ac
20	87	100.0	54	4	ABG65950 Rabbit ac
21	87	100.0	67	4	AB50037 Acetylcho
22	87	100.0	68	5	ABG31332 GFP-fused
23	87	100.0	348	8	ADL90218 Human enz
24	87	100.0	469	8	ABM83175 Human dia
25	87	100.0	500	2	AAW06990 Human ace

26	87	100.0	526	6	ABR38991	Abr38991 Human ace
27	87	100.0	526	8	ADR21588	Adr21588 Human enz
28	87	100.0	583	3	AAG80773	Aag80773 AChE prot
29	87	100.0	584	3	AAG80772	Aag80772 AChE prot
30	87	100.0	613	2	AAR06989	Aar06989 Human ace
31	87	100.0	614	2	AAR0726	Aar0726 Human ace
32	87	100.0	614	2	AAW49490	Aaw49490 Human ace
33	87	100.0	614	3	AAW49489	Aaw49489 Human wil
34	87	100.0	614	3	AAW49493	Aaw49493 Human ace
35	87	100.0	614	3	AAW49492	Aaw49492 Human ace
36	87	100.0	614	3	AAW49491	Aaw49491 Human ace
37	87	100.0	614	3	AAW49495	Aaw49495 Human ace
38	87	100.0	614	3	AAW49494	Aaw49494 Human ace
39	87	100.0	614	5	AAU11231	Aau11231 Human ace
40	87	100.0	614	5	AAU11232	Aau11232 Human ace
41	87	100.0	614	5	AAU11234	Aau11234 Human ace
42	87	100.0	614	5	AAU11233	Aau11233 Human ace
43	87	100.0	614	6	ABP59222	Abp59222 Human dru
44	87	100.0	614	6	ABP99726	Abp99726 Amino aci
45	87	100.0	614	7	ABG61695	Ade61695 Rat Prote
46	87	100.0	614	7	ADE61697	Ade61697 Human Pro
47	87	100.0	614	7	ADE61689	Ade61689 Human Pro
48	87	100.0	614	7	ADE61687	Ade61687 Rat Prote
49	87	100.0	614	7	ADE61683	Ade61683 Rat Prote
50	87	100.0	614	7	ADE61691	Ade61691 Rat Prote
51	87	100.0	614	7	ADE61693	Ade61693 Human Pro
52	87	100.0	614	7	ADE61685	Ade61685 Human Pro
53	87	100.0	614	8	ADQ89842	Adq89842 Antagonis
54	87	100.0	620	5	AAU11235	Aau11235 Human ace
55	84	96.6	14	5	ABG66007	Abg66007 Human ace
56	84	96.6	14	5	ABG66017	Abg66017 Human ace
57	84	96.6	14	5	ABG65988	Abg65988 Human ace
58	84	96.6	14	5	ABG66018	Abg66018 Human ace
59	84	96.6	14	5	ABG65989	Abg65989 Human ace
60	83	95.4	13	5	ABG66025	Abg66025 Human ace
61	83	95.4	14	5	ABG65983	Abg65983 Human ace
62	83	95.4	14	5	ABG65986	Abg65986 Human ace
63	83	95.4	14	5	ABG66021	Abg66021 Human ace
64	83	95.4	14	5	ABG66002	Abg66002 Human ace
65	82	94.3	13	5	ABG66035	Abg66035 Human ace
66	82	94.3	14	5	ABG66004	Abg66004 Human ace
67	82	94.3	14	5	ABG65981	Abg65981 Human ace
68	82	94.3	14	5	ABG66045	Abg66045 Human ace
69	82	94.3	14	5	ABG66024	Abg66024 Human ace
70	81	93.1	14	5	ABG66020	Abg66020 Human ace
71	81	93.1	14	5	ABG66015	Abg66015 Human ace
72	81	93.1	14	5	ABG66012	Abg66012 Human ace
73	80	92.0	14	5	ABG66005	Abg66005 Human ace
74	80	92.0	14	5	ABG66008	Abg66008 Human ace
75	80	92.0	14	5	ABG65984	Abg65984 Human ace
76	80	92.0	14	5	ABG65987	Abg65987 Human ace
77	80	92.0	14	5	ABG65990	Abg65990 Human ace
78	80	92.0	14	5	AAW39079	Aaw39079 Torpedo c
79	80	92.0	575	2	AAW39078	Aaw39078 Torpedo c
80	80	92.0	576	7	ABR4598	Abm4598 T califon
81	80	92.0	576	8	ADM42074	Adm42074 Torpedo c
82	80	92.0	576	8	ADM42073	Adm42073 Torpedo c
83	79	90.8	14	5	ABG66013	Abg66013 Human ace
84	79	90.8	14	5	ABG65980	Abg65980 Human ace
85	79	90.8	14	5	ABG66003	Abg66003 Human ace
86	78	89.7	12	5	ABG66046	Abg66046 Human ace
87	78	89.7	12	5	ABG66026	Abg66026 Human ace
88	78	89.7	14	5	ABG65991	Abg65991 Human ace
89	78	89.7	14	5	ABG66019	Abg66019 Human ace
90	78	89.7	27	4	AB48916	Ab48916 Human ace
91	78	89.7	27	4	AB50034	Ab50034 Acetylcho
92	77	88.5	14	5	ABG66011	Abg66011 Human ace
93	77	88.5	14	5	ABG66014	Abg66014 Human ace
94	77	88.5	14	5	ABG66022	Abg66022 Human ace
95	77	88.5	14	5	ABG66009	Abg66009 Human ace
96	77	88.5	14	5	ABG65998	Abg65998 Human ace
97	75	86.2	14	5	ABG66010	Abg66010 Human ace
98	75	86.2	14	5	ABG66006	Abg66006 Human ace

99	74	85.1	14	5	ABG65985	Abg65985 Human ace	172	62	71.3	574	5	AAO18962	Aao18962 Human but
100	74	85.1	14	5	ABG65992	Abg65992 Human ace	173	62	71.3	574	5	AAO18973	Aao18973 Human but
101	74	85.1	14	5	ABG65999	Abg65999 Human ace	174	62	71.3	574	5	AAO18976	Aao18976 Human but
102	73	83.9	14	5	ABG66023	Abg66023 Human ace	175	62	71.3	574	5	AAO18928	Aao18928 Human but
103	73	83.9	14	5	ABG66016	Abg66016 Human ace	176	62	71.3	574	5	AAO18966	Aao18966 Human but
104	72	82.8	11	5	ABG66027	Abg66027 Human ace	177	62	71.3	574	5	AAO18898	Aao18898 Human but
105	72	82.8	14	5	ABG65982	Abg65982 Human ace	178	62	71.3	574	6	ABR62391	AbR62391 Human but
106	71	81.6	12	5	ABG66036	Abg66036 Human ace	179	62	71.3	574	7	ABW00724	AbW00724 Human but
107	67	77.0	14	5	ABG66000	Abg66000 Human ace	180	62	71.3	574	7	ABW00695	AbW00695 Human but
108	65	74.7	574	5	AAO18903	Aao18903 Horse but	181	62	71.3	574	7	ABW00725	AbW00725 Human but
109	65	74.7	574	8	ADR01083	AdR01083 Rat butYr	182	62	71.3	574	7	ABW00722	AbW00722 Human but
110	64	73.6	10	5	ABG66028	Abg66028 Human ace	183	62	71.3	574	7	ABW00723	AbW00723 Human but
111	63	72.4	11	5	ABG66037	Abg66037 Human ace	184	62	71.3	574	7	ADP44756	AdP44756 Human but
112	62	71.3	10	5	ABG66047	Abg66047 Human ace	185	62	71.3	574	8	ADP44760	AdP44760 Human but
113	62	71.3	574	5	Aae25235	Aae25235 Human but	186	62	71.3	574	8	ADP44762	AdP44762 Human but
114	62	71.3	574	5	AAO18934	Aao18934 Human but	187	62	71.3	574	8	ADP44769	AdP44769 Human but
115	62	71.3	574	5	AAO18977	Aao18977 Human but	188	62	71.3	574	8	ADP44800	AdP44800 Human but
116	62	71.3	574	5	AAO18957	Aao18957 Human but	189	62	71.3	574	8	ADP44819	AdP44819 Human but
117	62	71.3	574	5	AAO18968	Aao18968 Human but	190	62	71.3	574	8	ADP44757	AdP44757 Human but
118	62	71.3	574	5	AAO18899	Aao18899 Human but	191	62	71.3	574	8	ADP44766	AdP44766 Human but
119	62	71.3	574	5	AAO18900	Aao18900 Human but	192	62	71.3	574	8	ADP44783	AdP44783 Human but
120	62	71.3	574	5	AAO18949	Aao18949 Human but	193	62	71.3	574	8	ADP44784	AdP44784 Human but
121	62	71.3	574	5	AAO18956	Aao18956 Human but	194	62	71.3	574	8	ADP44796	AdP44796 Human but
122	62	71.3	574	5	AAO18926	Aao18926 Human but	195	62	71.3	574	8	ADP44804	AdP44804 Human but
123	62	71.3	574	5	AAO18939	Aao18939 Human but	196	62	71.3	574	8	ADP44812	AdP44812 Human but
124	62	71.3	574	5	AAO18943	Aao18943 Human but	197	62	71.3	574	8	ADP44750	AdP44750 Human but
125	62	71.3	574	5	AAO18963	Aao18963 Human but	198	62	71.3	574	8	ADP44764	AdP44764 Human but
126	62	71.3	574	5	AAO18981	Aao18981 Human but	199	62	71.3	574	8	ADP44770	AdP44770 Human but
127	62	71.3	574	5	AAO18901	Aao18901 Human but	200	62	71.3	574	8	ADP44773	AdP44773 Human but
128	62	71.3	574	5	AAO18927	Aao18927 Human but	201	62	71.3	574	8	ADP44778	AdP44778 Human but
129	62	71.3	574	5	AAO18932	Aao18932 Human but	202	62	71.3	574	8	ADP44779	AdP44779 Human but
130	62	71.3	574	5	AAO18940	Aao18940 Human but	203	62	71.3	574	8	ADP44808	AdP44808 Human but
131	62	71.3	574	5	AAO18942	Aao18942 Human but	204	62	71.3	574	8	ADP44742	AdP44742 Human but
132	62	71.3	574	5	AAO18950	Aao18950 Human but	205	62	71.3	574	8	ADP44747	AdP44747 Human but
133	62	71.3	574	5	AAO18951	Aao18951 Human but	206	62	71.3	574	8	ADP44802	AdP44802 Human but
134	62	71.3	574	5	AAO18959	Aao18959 Human but	207	62	71.3	574	8	ADP44809	AdP44809 Human but
135	62	71.3	574	5	AAO18960	Aao18960 Human but	208	62	71.3	574	8	ADP44811	AdP44811 Human but
136	62	71.3	574	5	AAO18975	Aao18975 Human but	209	62	71.3	574	8	ADP44828	AdP44828 Human but
137	62	71.3	574	5	AAO18982	Aao18982 Human but	210	62	71.3	574	8	ADP44755	AdP44755 Human but
138	62	71.3	574	5	AAO18952	Aao18952 Human but	211	62	71.3	574	8	ADP44763	AdP44763 Human but
139	62	71.3	574	5	AAO18972	Aao18972 Human but	212	62	71.3	574	8	ADP44765	AdP44765 Human but
140	62	71.3	574	5	AAO18974	Aao18974 Human but	213	62	71.3	574	8	ADP44767	AdP44767 Human but
141	62	71.3	574	5	AAO18953	Aao18953 Human but	214	62	71.3	574	8	ADP44772	AdP44772 Human but
142	62	71.3	574	5	AAO18958	Aao18958 Human but	215	62	71.3	574	8	ADP44775	AdP44775 Human but
143	62	71.3	574	5	AAO18970	Aao18970 Human but	216	62	71.3	574	8	ADP44787	AdP44787 Human but
144	62	71.3	574	5	AAO18971	Aao18971 Human but	217	62	71.3	574	8	ADP44797	AdP44797 Human but
145	62	71.3	574	5	AAO18930	Aao18930 Human but	218	62	71.3	574	8	ADP44817	AdP44817 Human but
146	62	71.3	574	5	AAO18944	Aao18944 Human but	219	62	71.3	574	8	ADP44741	AdP44741 Human but
147	62	71.3	574	5	AAO18978	Aao18978 Human but	220	62	71.3	574	8	ADP44748	AdP44748 Human but
148	62	71.3	574	5	AAO18983	Aao18983 Human but	221	62	71.3	574	8	ADP44807	AdP44807 Human but
149	62	71.3	574	5	AAO18929	Aao18929 Human but	222	62	71.3	574	8	ADP44827	AdP44827 Human but
150	62	71.3	574	5	AAO18933	Aao18933 Human but	223	62	71.3	574	8	ADP44745	AdP44745 Human but
151	62	71.3	574	5	AAO18938	Aao18938 Human but	224	62	71.3	574	8	ADP44752	AdP44752 Human but
152	62	71.3	574	5	AAO18979	Aao18979 Human but	225	62	71.3	574	8	ADP44776	AdP44776 Human but
153	62	71.3	574	5	AAO18980	Aao18980 Human but	226	62	71.3	574	8	ADP44789	AdP44789 Human but
154	62	71.3	574	5	AAO18905	Aao18905 Rat butYr	227	62	71.3	574	8	ADP44792	AdP44792 Human but
155	62	71.3	574	5	AAO18945	Aao18945 Human but	228	62	71.3	574	8	ADP44799	AdP44799 Human but
156	62	71.3	574	5	AAO18967	Aao18967 Human but	229	62	71.3	574	8	ADP44813	AdP44813 Human but
157	62	71.3	574	5	AAO18902	Aao18902 Human but	230	62	71.3	574	8	ADP44824	AdP44824 Human but
158	62	71.3	574	5	AAO18935	Aao18935 Human but	231	62	71.3	574	8	ADP44826	AdP44826 Human but
159	62	71.3	574	5	AAO18947	Aao18947 Human but	232	62	71.3	574	8	ADP44829	AdP44829 Human but
160	62	71.3	574	5	AAO18965	Aao18965 Human but	233	62	71.3	574	8	ADP44740	AdP44740 Human but
161	62	71.3	574	5	AAO18937	Aao18937 Human but	234	62	71.3	574	8	ADP44751	AdP44751 Human but
162	62	71.3	574	5	AAO18948	Aao18948 Human but	235	62	71.3	574	8	ADP44768	AdP44768 Human but
163	62	71.3	574	5	AAO18954	Aao18954 Human but	236	62	71.3	574	8	ADP44781	AdP44781 Human but
164	62	71.3	574	5	AAO18955	Aao18955 Human but	237	62	71.3	574	8	ADP44788	AdP44788 Human but
165	62	71.3	574	5	AAO18936	Aao18936 Human but	238	62	71.3	574	8	ADP44739	AdP44739 Human but
166	62	71.3	574	5	AAO18941	Aao18941 Human but	239	62	71.3	574	8	ADP44746	AdP44746 Human but
167	62	71.3	574	5	AAO18961	Aao18961 Human but	240	62	71.3	574	8	ADP44759	AdP44759 Human but
168	62	71.3	574	5	AAO18964	Aao18964 Human but	241	62	71.3	574	8	ADP44771	AdP44771 Human but
169	62	71.3	574	5	AAO18969	Aao18969 Human but	242	62	71.3	574	8	ADP44786	AdP44786 Human but
170	62	71.3	574	5	AAO18931	Aao18931 Human but	243	62	71.3	574	8	ADP44810	AdP44810 Human but
171	62	71.3	574	5	AAO18946	Aao18946 Human but	244	62	71.3	574	8	ADP44814	AdP44814 Human but

245	62	71.3	574	8	ADP44831	Human but	318	62	71.3	602	3	AAV49487	Human but
246	62	71.3	574	8	ADP44754	Human but	319	62	71.3	602	3	AAV49479	Human but
247	62	71.3	574	8	ADP44758	Human but	320	62	71.3	602	3	AAV49478	Human but
248	62	71.3	574	8	ADP44790	Human but	321	62	71.3	602	3	AAV49483	Human but
249	62	71.3	574	8	ADP44794	Human but	322	62	71.3	602	3	AAV49473	Human but
250	62	71.3	574	8	ADP44821	Human but	323	62	71.3	602	3	AAV49488	Human but
251	62	71.3	574	8	ADP44639	Human but	324	62	71.3	602	3	AAV49471	Human will
252	62	71.3	574	8	ADP44743	Human but	325	62	71.3	602	3	AAV49475	Human but
253	62	71.3	574	8	ADP44749	Human but	326	62	71.3	602	3	AAV44573	Human will
254	62	71.3	574	8	ADP44795	Human but	327	62	71.3	602	3	AAV44574	Human but
255	62	71.3	574	8	ADP44822	Human but	328	62	71.3	602	5	AAO18897	Human but
256	62	71.3	574	8	ADP44833	Human but	329	62	71.3	602	5	AAO18897	Human but
257	62	71.3	574	8	ADP44744	Human but	330	62	71.3	602	7	ADP90908	Human hep
258	62	71.3	574	8	ADP44774	Human but	331	62	71.3	635	1	AAV60097	Sequence
259	62	71.3	574	8	ADP44791	Human but	332	62	71.3	635	2	AAV41509	Full-leng
260	62	71.3	574	8	ADP44793	Human but	333	59	67.8	9	5	ABG66029	Human ace
261	62	71.3	574	8	ADP44816	Human but	334	59	67.8	10	5	ABG66038	Human ace
262	62	71.3	574	8	ADP44830	Human but	335	59	67.8	14	5	ABG65993	Human ace
263	62	71.3	574	8	ADP44761	Human but	336	59	67.8	40	4	ABG62386	Alternati
264	62	71.3	574	8	ADP44777	Human but	337	58	66.7	14	5	ABG66001	Human ace
265	62	71.3	574	8	ADP44782	Human but	338	58	66.7	42	4	AAU04300	Human but
266	62	71.3	574	8	ADP44823	Human but	339	58	66.7	42	4	AAU04300	Human but
267	62	71.3	574	8	ADP44738	Human but	340	57	65.5	43	4	AAU05014	Mouse but
268	62	71.3	574	8	ADP44801	Human but	341	57	65.5	43	4	AAU05014	Mouse but
269	62	71.3	574	8	ADP44820	Human but	342	57	65.5	47	4	AAU05013	Rabbit bu
270	62	71.3	574	8	ADP44785	Human but	343	57	65.5	47	4	AAU05013	Rabbit bu
271	62	71.3	574	8	ADP44798	Human but	344	56	64.4	574	5	AAO18904	Cat butyr
272	62	71.3	574	8	ADP44803	Human but	345	56	64.4	574	8	ADR01082	Cat butyr
273	62	71.3	574	8	ADP44815	Human but	346	55	63.2	14	5	ABG65994	Human ace
274	62	71.3	574	8	ADP44818	Human but	347	54	62.1	9	5	ABG66039	Human ace
275	62	71.3	574	8	ADP44825	Human but	348	48	55.2	8	5	ABG66030	Human ace
276	62	71.3	574	8	ADP44753	Human but	349	48	55.2	8	5	ABG66048	Human ace
277	62	71.3	574	8	ADP44780	Human but	350	48	55.2	14	5	ABG65995	Human ace
278	62	71.3	574	8	ADP44805	Human but	351	47	54.0	8	5	ABG66040	Human ace
279	62	71.3	574	8	ADP44806	Human but	352	47	54.0	100	2	ADJ36833	Amino aci
280	62	71.3	574	8	ADR01039	Human but	353	47	54.0	583	8	ADJ33707	ACHE1 pro
281	62	71.3	574	8	ADR01077	Human but	354	46	52.9	288	6	ABU12110	Human pro
282	62	71.3	574	8	ADR01051	Human but	355	45	51.7	440	6	ABO00551	Novel hum
283	62	71.3	574	8	ADR01059	Human but	356	45	51.7	824	3	ABA42174	Human ORF
284	62	71.3	574	8	ADR01055	Human but	357	44	50.6	7	5	ABG66031	Human ace
285	62	71.3	574	8	ADR01079	Human but	358	44	50.6	473	5	ADN20823	Bacterial
286	62	71.3	574	8	ADR01045	Human but	359	43	49.4	7	5	ABG66041	Human ace
287	62	71.3	574	8	ADR01075	Human but	360	43	49.4	109	4	AAU60592	Propionib
288	62	71.3	574	8	ADR01053	Human but	361	43	49.4	109	6	ABM57111	Propionib
289	62	71.3	574	8	ADR01080	Human but	362	43	49.4	197	6	ABM69436	Photorhab
290	62	71.3	574	8	ADR01041	Human but	363	43	49.4	223	5	AAU49649	Human act
291	62	71.3	574	8	ADR01047	Human but	364	43	49.4	496	4	ABG23733	Novel hum
292	62	71.3	574	8	ADR01057	Human but	365	43	49.4	585	5	ABG91077	Herbicida
293	62	71.3	574	8	ADR01063	Human but	366	43	49.4	593	4	ABBS6290	Drocephal
294	62	71.3	574	8	ADR01067	Human but	367	42	48.3	67	6	ABM62632	Propionib
295	62	71.3	574	8	ADR01073	Human but	368	42	48.3	67	6	ABM62632	Propionib
296	62	71.3	574	8	ADR01061	Human but	369	42	48.3	119	6	ABO27172	Mouse ant
297	62	71.3	574	8	ADR01065	Human but	370	42	48.3	261	5	AAU49650	Canine ep
298	62	71.3	574	8	ADR01071	Human but	371	42	48.3	387	3	AAV99482	Jojoba ac
299	62	71.3	574	8	ADR01035	Human but	372	42	48.3	429	2	AAV60580	Human nor
300	62	71.3	574	8	ADR01043	Human but	373	42	48.3	657	3	AAV52193	Beta gluc
301	62	71.3	574	8	ADR01081	Human but	374	42	48.3	822	4	AAE01779	Human gen
302	62	71.3	574	8	ADR01037	Human but	375	42	48.3	822	4	AAE01851	Human gen
303	62	71.3	574	8	ADR01049	Human but	376	42	48.3	822	4	ABa47602	APC2. 1/2
304	62	71.3	574	8	ADR01069	Human but	377	42	48.3	822	5	ABG64185	Human alb
305	62	71.3	574	8	ADR01078	Human but	378	42	48.3	822	5	AAE24623	Human cul
306	62	71.3	574	8	AAV37442	Full-leng	379	42	48.3	822	6	ADA57244	Human sec
307	62	71.3	602	2	AAV37442	Full-leng	380	42	48.3	822	6	ADA41125	Human sec
308	62	71.3	602	3	AAV49486	Human but	381	42	48.3	822	7	ADC02487	Cullin AP
309	62	71.3	602	3	AAV49481	Human but	382	42	48.3	822	7	ADC74342	Human sec
310	62	71.3	602	3	AAV59235	Human but	383	42	48.3	822	7	ADP17872	Cullin AP
311	62	71.3	602	3	AAV49472	Human but	384	42	48.3	822	8	ADL77450	Albumin f
312	62	71.3	602	3	AAV49477	Human but	385	42	48.3	1578	7	ABM85515	Human pro
313	62	71.3	602	3	AAV49474	Human but	386	42	48.3	1784	8	ADP72342	Human sup
314	62	71.3	602	3	AAV49480	Human but	387	42	48.3	1788	2	AAV06077	Human act
315	62	71.3	602	3	AAV49484	Human but	388	42	48.3	1788	7	ADJ70459	Human hea
316	62	71.3	602	3	AAV49485	Human but	389	42	48.3	1789	7	ADE58829	Human Pro
317	62	71.3	602	3	AAV49482	Human but	390	42	48.3	1789	7	ADE58832	Human Pro
					AAV49476	Human but							

391	42	48.3	1792	2	AA0606078	AA06078 Bovine ac	464	39	44.8	109	4	AB011629	Ab011629 Human sec
392	42	48.3	2152	2	AB085514	Mouse pro	465	39	44.8	112	4	AB016780	Ab016780 Novel hum
393	42	48.3	2213	2	AA0606079	Human act	466	39	44.8	116	7	AB097826	Ab097826 HEV relat
394	41	47.1	73	4	AA084033	Human imm	467	39	44.8	121	7	AB075311	Ab075311 Murine an
395	41	47.1	83	4	AA076218	Human col	468	39	44.8	121	7	AB075296	Ab075296 Murine mo
396	41	47.1	95	4	AB0303475	Novel hum	469	39	44.8	121	7	AB075312	Ab075312 Murine an
397	41	47.1	95	4	AB060356	Human con	470	39	44.8	121	7	AB075315	Ab075315 Anti-CD22
398	41	47.1	234	6	AB024823	Protein e	471	39	44.8	121	7	AB075313	Ab075313 Murine an
399	41	47.1	327	4	AB080415	Gene #1 a	472	39	44.8	121	7	AB075314	Ab075314 Murine an
400	41	47.1	349	4	AB080414	Gene #1 a	473	39	44.8	121	8	AB079524	Ab079524 Anti-CD22
401	41	47.1	358	6	AB070568	Photorehab	474	39	44.8	121	8	AB079525	Ab079525 Anti-CD22
402	41	47.1	414	4	AB080371	Secreted	475	39	44.8	121	8	AB079526	Ab079526 Anti-CD22
403	41	47.1	414	5	AB065290	Human alb	476	39	44.8	121	8	AB079527	Ab079527 Humanised
404	41	47.1	414	6	ADA84087	Human RHL	477	39	44.8	121	8	AB079508	Ab079508 Murine an
405	41	47.1	414	8	ADL78557	Albumin f	478	39	44.8	121	8	AB079523	Ab079523 Anti-CD22
406	41	47.1	414	8	AD080374	HERV-H LT	479	39	44.8	124	2	AA075612	AA075612 VH Fab M5
407	41	47.1	511	8	ADN10581	Nicotiana	480	39	44.8	124	2	AA075572	AA075572 VH Fab 3b
408	41	47.1	511	8	ADN10583	Nicotiana	481	39	44.8	124	2	AA075615	AA075615 VH Fab M5
409	41	47.1	512	5	AB091556	Herbicida	482	39	44.8	124	2	AA075610	AA075610 VH Fab M5
410	40.5	46.6	166	7	ADH86122	Enterococ	483	39	44.8	124	2	AA075570	AA075570 VH Fab 3b
411	40.5	46.6	510	2	AA041195	Yeast del	484	39	44.8	124	2	AA075611	AA075611 VH Fab M5
412	40.5	46.6	510	3	AA070269	S. cerevi	485	39	44.8	124	2	AA075617	AA075617 VH Fab M5
413	40.5	46.6	510	8	AD043511	Bacterial	486	39	44.8	124	2	AA075613	AA075613 VH Fab M5
414	40	46.0	6	5	AB066032	Human ace	487	39	44.8	124	2	AA075616	AA075616 VH Fab M5
415	40	46.0	107	4	AA0522500	Propionib	488	39	44.8	124	2	AA075614	AA075614 VH Fab M5
416	40	46.0	116	3	AB049019	Propionib	489	39	44.8	137	2	AA062445	AA062445 81C6 heav
417	40	46.0	120	8	ADN48044	Thermococ	490	39	44.8	144	2	AA083446	AA083446 Heavy cha
418	40	46.0	120	8	ADN48044	Thermococ	491	39	44.8	151	4	AA090539	AA090539 C glutami
419	40	46.0	124	2	AA015441	Heavy cha	492	39	44.8	225	7	AB084151	AB084151 Pseudomon
420	40	46.0	124	2	AA054244	Anti-HIV	493	39	44.8	231	6	ABU43347	ABU43347 Protein e
421	40	46.0	124	2	AA054245	Anti-HIV	494	39	44.8	238	4	ABG24775	ABG24775 Novel hum
422	40	46.0	124	2	AA054246	Anti-HIV	495	39	44.8	238	6	ABU30084	ABU30084 Protein e
423	40	46.0	124	2	AA054335	Anti-HIV	496	39	44.8	238	7	ADC95792	ADC95792 E. faeciu
424	40	46.0	124	2	AA075568	VH Fab MT	497	39	44.8	239	5	ABP39320	ABP39320 Staphyloc
425	40	46.0	124	2	AA001246	VH region	498	39	44.8	250	3	AA044346	AA044346 3B3 antib
426	40	46.0	124	2	AA001227	VH region	499	39	44.8	256	3	AA094904	AA094904 Arabidops
427	40	46.0	124	2	AA001309	VH region	500	39	44.8	260	5	ABP45025	ABP45025 Human Bly
428	40	46.0	124	2	AA001247	VH region							
429	40	46.0	124	3	AA098207	Anti-gp12							
430	40	46.0	124	3	AA098206	Anti-gp12							
431	40	46.0	124	3	AA098208	Anti-gp12							
432	40	46.0	124	3	AA098270	Anti-gp12							
433	40	46.0	124	3	AA095097	Anti-gp12							
434	40	46.0	124	3	AA095098	Anti-gp12							
435	40	46.0	124	3	AA095161	Anti-gp12							
436	40	46.0	124	3	AA095099	Anti-gp12							
437	40	46.0	124	6	AA037618	Chimpanze							
438	40	46.0	146	2	AA001228	VH region							
439	40	46.0	146	3	AA098285	Modified							
440	40	46.0	146	3	AA095176	Modified							
441	40	46.0	146	7	AD06734	Human IgG							
442	40	46.0	186	8	AD052392	Human ant							
443	40	46.0	243	5	ABP45395	Human Bly							
444	40	46.0	243	7	ADG96222	Single ch							
445	40	46.0	247	5	ABP45373	Human Bly							
446	40	46.0	247	7	ADG96200	Single ch							
447	40	46.0	257	7	ADJ72368	Human ant							
448	40	46.0	413	7	ADJ05750	Bacterial							
449	40	46.0	471	6	ABU19549	Protein e							
450	40	46.0	476	4	ABR61564	Human MAb							
451	40	46.0	549	4	ABR71550	Drosophil							
452	40	46.0	587	8	ADH62812	Lactobaci							
453	40	46.0	593	8	ADH62811	Lactobaci							
454	40	46.0	735	7	ADN05741	Human pro							
455	39.5	45.4	339	7	ADK19806	Human man							
456	39.5	45.4	611	4	ABU52898	Human met							
457	39.5	45.4	611	7	ADK19800	Human man							
458	39.5	45.4	618	8	ADJ92351	Human N-1							
459	39.5	45.4	6938	8	ADN96830	Bugula br							
460	39	44.8	6	5	ABG66042	Human ace							
461	39	44.8	68	4	AA094177	Human tes							
462	39	44.8	68	4	AB095638	Human tes							
463	39	44.8	96	4	AA084483	Human imm							

ALIGNMENTS

RESULT 1

AAW35340 standard; peptide; 14 AA.

ID AAW35340

AC AAW35340;

XX

DT 17-APR-1998 (first entry)

XX

XX Human acetylcholinesterase 14-mer peptide.

DE

XX

KW Acetylcholinesterase; AChE; neuronal degeneration; Parkinson's disease;

KW Alzheimer's disease; stroke; cancer; calcium channel modulator; antibody;

XX inhibitor.

XX

OS Homo sapiens.

XX

FN WO9735962-A1.

XX

XX 02-OCT-1997.

XX

XX 21-MAR-1997; 97WO-GB000796.

XX

PR 22-MAR-1996; 96GB-00006040.

XX

XX (ISIS-) ISIS INNOVATION LTD.

XX

XX Greenfield SA, Vaux DJ;

XX

XX WPI; 1997-489626/45.

XX

XX Peptide(s) from acetylcholine esterase which open calcium channels - used

PT for treating disorders of the central nervous system, cancer and stroke.

XX Claim 1; Page 20; 27pp; English.

XX This 14-mer peptide corresponds to residues 535-548 of the

XX Acetylcholinesterase mature protein. This peptide is known to act alone

XX or in synergism with a fragment of beta-amyloid to contribute to neuronal

XX degeneration. Compounds that inhibit the biological activity of the novel

XX peptides, and antibodies, can be used to control cytoplasmic calcium ion

XX currents in vivo, and are useful for treating disorders of the central

XX nervous system (e.g. Parkinson's and Alzheimer's diseases), stroke and

XX cancer

XX Sequence 14 AA;

Query Match 100.0%; Score 87; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVMVHWK 14

Db 1 AEFHRWSSYVMVHWK 14

RESULT 2

AAU04701

ID AAU04701 standard; peptide; 14 AA.

XX AAU04701;

XX 26-SEP-2001 (first entry)

XX Scrambled acetylcholinesterase (AChE) fragment.

XX Acetylcholinesterase; AChE; neurodegenerative disease; brain;

XX neurological disorder; Alzheimer's disease; Parkinson's disease;

XX motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;

XX hippocampal dysfunction.

XX Synthetic.

XX WO200149107-A1.

XX 12-JUL-2001.

XX 22-DEC-2000; 2000WO-GB004991.

XX 30-DEC-1999; 99GB-00030825.

XX (SYNA-) SYNAPTICA LTD.

XX Greenfield SA, Rawlins JNP, Deacon RMJ;

XX WPI; 2001-441761/47.

XX Providing animal model for Alzheimer's disease comprises introducing

XX peptide fragment from close to C-terminus of acetylcholine esterase which

XX causes cellular degeneration and impairment of testable brain function.

XX Example 3; Page 25; 44pp; English.

XX The sequence represents the amino acid sequence of a scrambled

XX acetylcholinesterase (AChE) fragment. The peptide is used in a method of

XX providing an animal model for a neurodegenerative disease. This involves

XX introducing the peptide fragment, from close to the C-terminus of AChE,

XX or an active variant of the peptide, into one or more sites in the brain

XX of a non-human animal, whereby the peptide causes cellular degeneration

XX and leads to impairment of testable brain function that is indicative of

XX a neurological disorder in a human. The animal model is useful for

XX testing an agent for biological activity in a neurodegenerative disorder

XX which involves administering the agent to a model for Alzheimer's disease

XX and determining whether the agent will inhibit, prevent or decrease

XX impairment of the testable brain function (cognitive function) and/or

CC cause improvement or deterioration of cellular damage in the brain. The

CC animal models are also useful as a model for Parkinson's disease, motor

CC neuron disease and prion-related diseases and thus for testing reagents

CC to assess their potential for treatment of Parkinson's disease. The AChE

CC peptide causes considerable nervous system damage, which is an order of

CC magnitude greater than that of the neurotoxin MDA (N-methyl-D-

CC aspartate). The lesions produced can be identified using simple

CC behavioral tests known to be affected by hippocampal dysfunction

XX Sequence 14 AA;

Query Match 100.0%; Score 87; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVMVHWK 14

Db 1 AEFHRWSSYVMVHWK 14

RESULT 3

ABG65979

ID ABG65979 standard; peptide; 14 AA.

XX ABG65979;

XX 28-AUG-2002 (first entry)

XX Human acetylcholinesterase (AChE) Synaptica peptide.

XX Human; acetylcholinesterase; Synaptica peptide; enzyme; AChE; amyloid;

XX acetylcholinesterase; fibril formation; surface tension; neuroprotective;

XX Alzheimer's disease; Parkinson's disease; motor neuron disease;

XX antiparkinsonian; nootropic.

XX Homo sapiens.

XX WO200242778-A2.

XX 30-MAY-2002.

XX 23-NOV-2001; 2001WO-GB005189.

XX 23-NOV-2000; 2000GB-00028578.

XX (SYNA-) SYNAPTICA LTD.

XX Vaux DJT, Cottingham MG, Voskuil JLA;

XX WPI; 2002-471743/50.

XX Novel use of the 14 mer synaptica peptide, or its amyloidogenic variant

XX capable of fibril formation, in screening a compound for ability to

XX inhibit amyloid-type fibril formation by the peptide.

XX Claim 1; Page 31; 41pp; English.

XX The invention relates to use of the 14 mer Synaptica peptide (an active

XX fragment of acetylcholinesterase) or its amyloidogenic variant capable of

XX fibril formation, in screening a compound for ability to inhibit amyloid-

XX type fibril formation by the Synaptica peptide. The peptide is useful for

XX screening a compound for the ability to inhibit amyloid-type fibril

XX formation, for preparing a compound by identifying an inhibitor of fibril

XX formation and for determining whether a peptide or polypeptide or a

XX variant is an amyloidogenic analogue of the Synaptica peptide. The

XX peptide is also useful for determining whether variants will decrease

XX surface tension in aqueous solution. The compounds detected are used for

XX treating Alzheimer's disease, Parkinson's disease and motor neuron

XX disease. Sequences ABG65979-ABG66050 represent human Synaptica peptide

XX variants of the invention

XX Sequence 14 AA;

```

Query Match      100.0%; Score 87; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMWVHWK 14
DB 1 AEFHRWSSYMWVHWK 14

RESULT 4
AAR77010
ID AAR77010 standard; protein; 39 AA.
XX
AC AAR77010;
XX
DT 31-MAR-1996 (first entry)
XX
DE Alternative human acetylcholinesterase (AChE) protein.
XX
KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7; chromosome-7q22;
KW acetylcholine-hydrolyzing enzyme.
XX
OS Homo sapiens.
XX
PN WO9523158-A1.
XX
PD 31-AUG-1995.
XX
PF 28-FEB-1995; 95WO-US002806.
XX
PR 28-FEB-1994; 94US-00202755.
PR 09-JAN-1995; 95US-00370156.
XX
PA (YISS ) YISSUM RES & DEV CO.
PA (KOHN/) KOHN K I.
XX
PI Soreq H, Zakut H, Shani M;
XX
WPI; 1995-311499/40.
XX
PT Alternative forms of human acetyl cholinesterase (ChE) gene - expressed
PT in transgenic animal assay system for evaluating anti-ChE activity of
PT organo:phosphate(s), etc. or as model of ChE imbalance.
XX
PS Disclosure; Fig 6; 55pp; English.
XX
CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at neuromuscular
CC junctions where it serves a vital function in modulating cholinergic
CC neurotransmission. This alternatively spliced form of human AChE may be
CC expressed in transgenic animals which are used in an assay system for
CC determining the anti-ChE activity of organophosphates, carbamates, anti-
CC ChE drugs, plant glycoalkaloids and snake venoms
XX
SQ Sequence 39 AA;

Query Match      100.0%; Score 87; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMWVHWK 14
DB 11 AEFHRWSSYMWVHWK 24

RESULT 5
AAB48915
ID AAB48915 standard; peptide; 40 AA.
XX
AC AAB48915;
XX
DT 16-MAR-2001 (first entry)
XX
DE Human acetylcholinesterase (AChE) C-terminal peptide, SEQ ID NO:2.

XX Acetylcholinesterase; AChE; splice variant; human; epitope;
KW C-terminal peptide; antibody; central nervous system; CNS stress;
KW psychological insult; physical insult; chemical insult;
KW blood-brain barrier disruption; elevated glucocorticoid level;
KW Alzheimer's disease; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200073343-A2.
XX
PD 07-DEC-2000.
XX
PF 31-MAY-2000; 2000WO-IL000312.
XX
PR 31-MAY-1999; 99IL-00130225.
XX
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Kaufer D, Friedman A, Seidman S;
XX
WPI; 2001-061514/07.
XX
PT Antibody specific to acetylcholinesterase or its C-terminal peptide
PT derivative useful for diagnosing, ventral nervous system stress, elevated
PT glucocorticoid level, disruption of blood-brain barrier and Alzheimer's
PT disease.
XX
PS Claim 4; Page 43; 44pp; English.
XX
CC The invention relates to antibodies which recognise acetylcholinesterase
CC (AChE) or a C-terminal peptide thereof (particularly AAB48914-B48916).
CC The AChE splice variant, AChE-R, and AChE-R mRNA, have been found to be
CC elevated in response to central nervous system (CNS) insults. The
CC invention therefore also relates to a method for diagnosing CNS stress,
CC and also elevated glucocorticoid levels, disruption of the blood-brain
CC barrier or Alzheimer's disease using a sample (e.g., serum or
CC cerebrospinal fluid) and an antibody of the invention. The CNS stress
CC which may be diagnosed using the antibodies is preferably that caused by
CC psychological insult, physical insult (head injury, head trauma, or
CC exposure to irradiation) or chemical insult (exposure to insecticide or
CC nerve gas). The present sequence represents a human AChE C-terminal
CC peptide which is specifically claimed as an epitope which is recognised
CC by an antibody of the invention
XX
SQ Sequence 40 AA;

Query Match      100.0%; Score 87; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMWVHWK 14
DB 12 AEFHRWSSYMWVHWK 25

RESULT 6
AAB50033
ID AAB50033 standard; peptide; 40 AA.
XX
AC AAB50033;
XX
DT 14-MAR-2001 (first entry)
XX
DE Acetylcholinesterase synaptic peptide ASP-1.
XX
KW ASP-1; haemostatic; acetylcholinesterase; AChE; cell growth; human;
KW cell differentiation; thrombocytopenia; post-irradiation condition;
KW post-chemotherapy condition; blood loss; stress-induced male infertility.
XX
OS Homo sapiens.
XX
PN WO200073427-A2.

```

XX 07-DEC-2000.
 XX 31-MAY-2000; 2000WO-IL000311.
 XX 31-MAY-1999; 99IL-00130224.
 XX 02-SEP-1999; 99IL-00131707.
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX Soreq H, Eldor A, Deutch V, Grisaru D;
 XX WPI; 2001-061523/07.
 XX New regulatory peptides having cell growth and cell differentiation
 PT activity derived from the C-terminal region of acetylcholinesterase
 PT useful in promoting growth, survival and differentiation of stem cells.
 XX
 XX Claim 8; Page 50; 133pp; English.
 XX The present sequence is a C-terminal peptide of acetylcholinesterase
 CC (AChE). This peptide is acetylcholinesterase "synaptic" peptide (ASP-1).
 CC This peptide has a cell growth and/or cell differentiation activity. The
 CC peptide may be used in ex vivo or in vivo expansion of haematopoietic
 CC stem cells and neural progenitors, and in the promotion of megakaryocytic
 CC differentiation of hematopoietic stem cells. In addition, the present
 CC peptide may be used in for promoting expansion of committed neural
 CC progenitors in a developing embryo, in cultured embryonic stem cells, and
 CC embryoid bodies derived from them. The present peptide may further be
 CC used in the treatment of thrombocytopenia, post-irradiation conditions,
 CC post-chemotherapy conditions, and conditions following massive blood
 CC loss, in inducing synthesis of AChE mRNA, and in promoting formation of
 CC hematoid bodies. Antibodies directed against the present peptide are
 CC useful for diagnosing stress-induced male infertility
 XX
 XX Sequence 40 AA;
 SQ Query Match 100.0%; Score 87; DB 4; Length 40;
 Best Local Similarity 100.0%; Pred. No. 8.5e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEFHRWSSYMYHWK 14
 |||||
 Db 12 AEFHRWSSYMYHWK 25
 RESULT 7
 AAU98023
 ID AAU98023 standard; peptide; 40 AA.
 XX AAU98023;
 XX 27-AUG-2002 (first entry)
 XX Human synaptic acetylcholinesterase unique region.
 DE Human; acetylcholinesterase; single-chain variable fragment; synaptic;
 XX scFv; AChE-S; heavy chain variable region; muscle re-innervation;
 KW progressive neuromuscular disorder; muscle distortion; myasthenia gravis;
 KW neuromuscular junction abnormality; Eaton-Lambert disease;
 KW muscular dystrophy; amyotrophic lateral sclerosis; ALS;
 KW post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
 KW post-stroke sclerosis; post-injury muscle damage;
 XX excessive re-innervation.
 XX Homo sapiens.
 OS
 XX WO200246422-A1.
 PN 13-JUN-2002.
 XX 22-MAY-2001; 2001WO-IL000464.
 XX

PR 04-DEC-2000; 2000IL-00140071.
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX Soreq H, Flores CF, Nissim A;
 XX WPI; 2002-463832/49.
 XX Nucleic acid sequence coding for a single-chain variable fragment (scFv)
 PT antibody that has specific affinity for the synaptic variant of
 PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular
 PT disorder, e.g. Myasthenia gravis.
 XX
 XX Disclosure; Fig 1; 73pp; English.
 XX The invention relates to a nucleic acid sequence coding for a single-
 CC chain variable fragment (scFv) antibody that has specific affinity for
 CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv
 CC antibody consists essentially of a polypeptide comprising the binding
 CC portion of the heavy chain variable region of an antibody. Also included
 CC are an expression vehicle comprising a nucleic acid sequence coding for a
 CC scFv antibody that has specific affinity for the synaptic variant of AChE
 CC -S, an scFv antibody specifically recognising and binding to the synaptic
 CC variant of AChE-S and a method for the diagnosis of a progressive
 CC neuromuscular disorder in a mammal, comprising obtaining a sample from
 CC the mammal and detecting intensified expression of at least one of the
 CC AChE variants in the sample. The single-chain Fv antibody is useful for
 CC diagnosing a progressive neuromuscular disorder which involves any one of
 CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
 CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
 CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
 CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post
 CC -stroke sclerosis, post-injury muscle damage, excessive re-innervation,
 CC or post-exposure to AChE inhibitors. The present sequence represents the
 CC unique region of human acetylcholinesterase encoded by a synaptically
 CC expressed splice variant
 XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 87; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 8.5e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEFHRWSSYMYHWK 14
 |||||
 Db 12 AEFHRWSSYMYHWK 25
 RESULT 8
 AAU04705
 ID AAU04705 standard; peptide; 44 AA.
 XX AAU04705;
 XX 26-SEP-2001 (first entry)
 XX Rat acetylcholinesterase (AChE) fragment.
 DE Acetylcholinesterase; AChE; neurodegenerative disease; brain;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;
 KW motor neuron disease; prion-related disease; NMJ; N-methyl-D-aspartate;
 KW hippocampal dysfunction; rat.
 XX Rattus sp.
 OS
 XX WO200149107-A1.
 PN 12-JUL-2001.
 XX 22-DEC-2000; 2000WO-GB004991.
 XX 30-DEC-1999; 99GB-00030825.
 XX

PT Providing animal model for Alzheimer's disease comprises introducing
 PT peptide fragment from close to C-terminus of acetylcholine esterase which
 PT causes cellular degeneration and impairment of testable brain function.

PS Disclosure; Fig 1; 44pp; English.

XX
 CC The sequence represents the amino acid sequence of a biologically active
 CC fragment of human acetylcholinesterase (AChE). The peptide is used in a
 CC method of providing an animal model for a neurodegenerative disease. This
 CC involves introducing the peptide fragment, from close to the C-terminus
 CC of AChE, or an active variant of the peptide, into one or more sites in
 CC the brain of a non-human animal, whereby the peptide causes cellular
 CC degeneration and leads to impairment of testable brain function that is
 CC indicative of a neurological disorder in a human. The animal model is
 CC useful for testing an agent for biological activity in a
 CC neurodegenerative disorder which involves administering the agent to a
 CC model for Alzheimer's disease and determining whether the agent will
 CC inhibit, prevent or decrease impairment of the testable brain function
 CC (cognitive function) and/or cause improvement or deterioration of
 CC cellular damage in the brain. The animal models are also useful as a
 CC model for Parkinson's disease, motor neuron disease and prion-related
 CC diseases and thus for testing reagents to assess their potential for
 CC treatment of Parkinson's disease. The AChE peptide causes considerable
 CC nervous system damage, which is an order of magnitude greater than that
 CC of the neurotoxin MNDA (N-methyl-D-aspartate). The lesions produced can
 CC be identified using simple behavioral tests known to be affected by
 CC hippocampal dysfunction

XX Sequence 44 AA;

Query Match 100.0%; Score 87; DB 4; Length 44;

Best Local Similarity 100.0%; Pred. No. 9.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSSYMVHWK 14

Db 16 AEFHRSSSYMVHWK 29

RESULT 11

AAG5951
 ID AAG65951 standard; protein; 44 AA.

XX AC AAG65951;

XX 11-FEB-2002 (first entry)

XX Mouse acetylcholinesterase (AChE) partial sequence.

XX Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
 KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
 KW Parkinson's disease; motor neuron disease.

XX Mus sp.

XX Key Location/Qualifiers
 FT Peptide 16..29
 FT /note= "synaptica peptide"

XX WO200173446-A1.

XX 04-OCT-2001.

XX 29-MAR-2001; 2001WO-GB001401.

XX 29-MAR-2000; 2000GB-00007630.

XX 15-DEC-2000; 2000GB-00030660.

XX (SYNA-) SYNAPTICA LTD.

XX Westwell M, Greenfield SA;

XX WPI; 2001-639255/73.

XX Use of alpha 7 nicotinic receptor or its functional analog to determine
 PT if a compound is capable of acting as functional analog or antagonist of
 PT acetylcholinesterase polypeptide for treating neurological disorders.

PS Disclosure; Fig 1; 45pp; English.

XX The invention relates to the use of an alpha 7 nicotinic receptor (I) or
 CC its functional analog to determine whether a compound is capable of
 CC acting as a functional analog or antagonist of an acetylcholinesterase
 CC (AChE) polypeptide fragment (synaptica peptide) on (I). If (I) is a
 CC native alpha 7 nicotinic receptor in its normal membrane environment, it
 CC is identified by means of inhibition by a blocker of (I). Methods for
 CC identifying a functional analog or antagonist of the synaptica peptide
 CC are also provided. The identified functional analog or antagonist is
 CC useful for the preparation of a medicament for treatment of a
 CC neurological disorder associated with non-enzymatic action of AChE, where
 CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
 CC motor neuron disease. It is useful for inhibiting or preventing non-
 CC enzymatic activity of the synaptica peptide in vivo. The present sequence
 CC represents the partial sequence of mouse AChE polypeptide containing the
 CC synaptica peptide fragment

XX Sequence 44 AA;

Query Match 100.0%; Score 87; DB 4; Length 44;

Best Local Similarity 100.0%; Pred. No. 9.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSSYMVHWK 14

Db 16 AEFHRSSSYMVHWK 29

RESULT 12

AAG5949

ID AAG65949 standard; protein; 44 AA.

XX AC AAG65949;

XX 11-FEB-2002 (first entry)

XX Human acetylcholinesterase (AChE) partial sequence.

XX Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
 KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
 KW Parkinson's disease; motor neuron disease.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 16..29
 FT /note= "synaptica peptide"

XX WO200173446-A1.

XX 04-OCT-2001.

XX 29-MAR-2001; 2001WO-GB001401.

XX 29-MAR-2000; 2000GB-00007630.

XX 15-DEC-2000; 2000GB-00030660.

XX (SYNA-) SYNAPTICA LTD.

XX Westwell M, Greenfield SA;

XX WPI; 2001-639255/73.

XX Use of alpha 7 nicotinic receptor or its functional analog to determine
 PT if a compound is capable of acting as functional analog or antagonist of
 PT acetylcholinesterase polypeptide for treating neurological disorders.

PS Disclosure; Fig 1; 45pp; English.

XX The invention relates to the use of an alpha 7 nicotinic receptor (I) or
 CC its functional analog to determine whether a compound is capable of
 CC acting as a functional analog or antagonist of an acetylcholinesterase
 CC (AChE) polypeptide fragment (synaptica peptide) on (I). If (I) is a
 CC native alpha 7 nicotinic receptor in its normal membrane environment, it
 CC is identified by means of inhibition by a blocker of (I). Methods for
 CC identifying a functional analog or antagonist of the synaptica peptide
 CC are also provided. The identified functional analog or antagonist is
 CC useful for the preparation of a medicament for treatment of a
 CC neurological disorder associated with non-enzymatic action of AChE, where
 CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
 CC motor neuron disease. It is useful for inhibiting or preventing non-
 CC enzymatic activity of the synaptica peptide in vivo. The present sequence
 CC represents the partial sequence of human AChE polypeptide containing the
 CC synaptica peptide fragment

XX Sequence 44 AA;

Query Match 100.0%; Score 87; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 DB 16 AEFHRWSSYVHWK 29
 |||||

RESULT 13
 AAG65952
 ID AAG65952 standard; protein; 44 AA.
 AC AAG65952;
 XX 11-FEB-2002 (first entry)

DE Rat acetylcholinesterase (AChE) partial sequence.
 XX Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
 KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
 KW Parkinson's disease; motor neuron disease.
 XX Rattus sp.
 XX Key Location/Qualifiers
 FT Peptide 16..29
 FT /note= "synaptica peptide"
 XX WO200173446-A1.
 XX 04-OCT-2001.
 XX 29-MAR-2001; 2001WO-GB001401.
 XX 29-MAR-2000; 2000GB-00007630.
 XX 15-DEC-2000; 2000GB-00030660.
 XX (SYNA-) SYNAPTICA LTD.
 XX Westwell M, Greenfield SA;
 XX WPI; 2001-639255/73.
 XX Use of alpha 7 nicotinic receptor or its functional analog to determine
 PT if a compound is capable of acting as functional analog or antagonist of
 PT acetylcholinesterase polypeptide for treating neurological disorders.
 XX Disclosure; Fig 1; 45pp; English.

XX The invention relates to the use of an alpha 7 nicotinic receptor (I) or
 CC its functional analog to determine whether a compound is capable of
 CC acting as a functional analog or antagonist of an acetylcholinesterase

CC (AChE) polypeptide fragment (synaptica peptide) on (I). If (I) is a
 CC native alpha 7 nicotinic receptor in its normal membrane environment, it
 CC is identified by means of inhibition by a blocker of (I). Methods for
 CC identifying a functional analog or antagonist of the synaptica peptide
 CC are also provided. The identified functional analog or antagonist is
 CC useful for the preparation of a medicament for treatment of a
 CC neurological disorder associated with non-enzymatic action of AChE, where
 CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
 CC motor neuron disease. It is useful for inhibiting or preventing non-
 CC enzymatic activity of the synaptica peptide in vivo. The present sequence
 CC represents the partial sequence of rat AChE polypeptide containing the
 CC synaptica peptide fragment

XX Sequence 44 AA;

Query Match 100.0%; Score 87; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.3e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 DB 16 AEFHRWSSYVHWK 29
 |||||

RESULT 14
 AAW74586
 ID AAW74586 standard; protein; 45 AA.
 AC AAW74586;
 XX 21-DEC-1998 (first entry)

DE Amino acid sequence of the human AChE variant 1.
 XX Nuclease resistance; inhibition; human; acetylcholinesterase; AChE;
 KW central nervous system; CNS.
 XX Homo sapiens.
 XX WO9839486-A1.
 XX 11-SEP-1998.
 XX 06-MAR-1998; 98WO-US004503.
 XX 06-MAR-1997; 97US-0040203P.
 XX (YISS) YISSUM RES & DEV CO.
 XX (KOHN/) KOHN K I.
 XX Soreq H, Seidman S, Shohami E;
 XX WPI; 1998-506377/43.
 XX Treatment of injury to central nervous system - by administration of
 XX inhibitor of acetylcholinesterase production.
 XX Disclosure; Page 61; 88pp; English.

XX This is the amino acid sequence of a human acetylcholinesterase (AChE)
 CC variant used in the method of the invention, where inhibitors of AChE are
 CC used to treat injury to the central nervous system (CNS). The AChE
 CC inhibitor can also be used to facilitate transplantation of neuronal
 CC cells to the CNS of a patient. The inhibitor can also be used to improve
 CC hippocampal neuron survival following injury to the CNS. The CNS injuries
 CC that can be treated with the method include epilepsy, stroke,
 CC Huntington's disease, head injury, spinal injury, pain, Parkinson's
 CC disease, myelin deficiencies, neuromuscular disorders, neurological pain,
 CC amyotrophic lateral sclerosis, Alzheimer's disease, and affective
 CC disorders of the brain

XX Sequence 45 AA;

Query Match 100.0%; Score 87; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 17 AEFHRWSSYVHWK 30

RESULT 15
 AAW48800
 ID AAW48800 standard; protein; 45 AA.
 XX
 AC AAW48800;
 XX
 DT 07-OCT-1998 (first entry)
 XX
 DE C-terminal fragment of human acetylcholine esterase variant E1-4, 6.
 XX
 KW Human acetylcholine esterase-I4 readthrough splice variant; AChE-I4; CNS;
 KW blood/brain barrier; BBB; I4 peptide; antibiotic; brain tumour; glioma;
 KW chemotherapeutic drug; central nervous system.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..5
 FT FT /note= "This region is encoded by the 3' end of AChE exon 4"
 FT FT
 FT Region 6..45
 FT FT /note= "Residues encoded by AChE exon 6"
 FT FT
 XX WO9822132-A2.
 XX
 XX 28-MAY-1998.
 XX
 XX 20-NOV-1997; 97WO-US021696.
 XX
 PR 20-NOV-1996; 96US-0031194P.
 PR 12-DEC-1996; 96US-0035266P.
 PR 21-JUL-1997; 97US-0053200P.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 PA (KOHN/) KOHN K I.
 XX
 PI Soreq H, Friedman A, Seidman S, Kaufers D;
 XX
 XX WPI; 1998-312172/27.
 XX
 PT Increasing the permeability of the blood/brain barrier - using e.g.
 PT adrenaline, atropine or acetylcholine esterase I4 splice variant peptide,
 PT useful for imaging and/or treatment of central nervous system disorders.
 XX
 XX Disclosure; Fig 2; 71pp; English.
 XX
 CC The present sequence represents a C-terminal fragment of the human
 CC acetylcholine esterase splice variant E1-4, 6. The AChE E1-4, 6 variant
 CC comprises of residues encoded by exons 1-4 of AChE linked to residues
 CC encoded by the alternatively spliced AChE exon 6. The invention claims
 CC for the human acetylcholine esterase-I4 (AChE-I4) readthrough splice
 CC variant (AAW48797). The invention provides a pharmaceutical composition,
 CC for facilitating passage of compounds through the blood/brain barrier
 CC (BBB), comprising of AChE-I4, I4 peptide (see AAW48797) or AChE-I4
 CC analogues (such as the AChE E1-4, 6 variant) together with a
 CC pharmaceutically acceptable carrier. The pharmaceutical composition is
 CC claimed to facilitate a reversible disruption of the BBB allowing
 CC transport of compounds through the BBB. The compounds, e.g. imaging
 CC agents, antibiotics or chemotherapeutic drugs, are claimed to be useful
 CC for the diagnosis and treatment of diseases or disorders of the CNS such
 CC as infections, neurochemical disorders, brain tumours, gliomas, etc

Query Match 100.0%; Score 87; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 17 AEFHRWSSYVHWK 30

RESULT 16
 AAW68144
 ID AAW68144 standard; protein; 45 AA.
 XX
 AC AAW68144;
 XX
 DT 05-OCT-1998 (first entry)
 XX
 DE Human AChE splice variant E1-4, 6.
 XX
 KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis; AChE;
 KW Parkinson's disease; Alzheimer's disease; central nervous system;
 KW neuromuscular junction; cholinergic signalling; brain.
 XX
 OS Homo sapiens.
 XX
 FN WO9826062-A2.
 XX
 PD 18-JUN-1998.
 XX
 PP 12-DEC-1997; 97WO-US023598.
 XX
 PR 12-DEC-1996; 96US-0035266P.
 PR 13-FEB-1997; 97US-0037777P.
 PR 02-MAY-1997; 97US-00850347.
 PR 21-JUL-1997; 97US-0053334P.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 PA (KOHN/) KOHN K I.
 XX
 PI Soreq H, Seidman S, Eckstein F, Friedman A, Kaufers D;
 XX
 XX WPI; 1998-348522/30.
 XX
 PT Synthetic nuclease resistant antisense oligodeoxynucleotides - directed
 PT against acetylcholinesterase, useful for treating Parkinson's and
 PT Alzheimer's diseases and myasthenia gravis.
 XX
 XX Disclosure; Fig 12; 89pp; English.
 XX
 CC This represents the amino acid sequence of a human acetylcholinesterase
 CC (AChE) splice variant. The invention provides sequences shown in AAV41278
 CC to AAV41285 that represent synthetic nuclease resistant antisense
 CC oligodeoxynucleotides which are capable of selectively modulating human
 CC acetylcholinesterase (AChE) production. These oligonucleotides are
 CC targeted to a splice junction in a splice variant of AChE mRNA and are
 CC capable of selectively modulating human AChE production in the central
 CC nervous system and neuromuscular junction. The invention also provides a
 CC method for determining the efficacy of these human AChE specific
 CC antisense oligonucleotides. These antisense oligonucleotides can be used
 CC to restore balanced cholinergic signalling in the brain, particularly
 CC related to learning and memory as well as stress disorders, Parkinson's
 CC and Alzheimer's disease. They can also be used to reduce production and
 CC therefore deposition of AChE in the neuromuscular junctions of patients
 CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low
 CC doses while avoiding many of the side effects associated with Tacrine and
 CC related cholinergic drugs for Alzheimer's disease and pyridostigmine and
 CC related drugs for myasthenia gravis

Query Match 100.0%; Score 87; DB 2; Length 45;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 17 AEFHRWSSYVHWK 30

Sequence 45 AA;

```

QY      1 AEFHRWSSYVHWK 14
      |||||||
Db      17 AEFHRWSSYVHWK 30

RESULT 17
AAU04299
ID      AAU04299 standard; peptide; 53 AA.
XX
XX      AC      AAU04299;
XX
XX      DT      26-SEP-2001 (first entry)
XX
XX      DE      Bovine acetylcholinesterase (AChE) fragment.
XX
XX      KW      Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW      neurological disorder; Alzheimer's disease; Parkinson's disease;
KW      motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW      hippocampal dysfunction; bovine.
XX
XX      OS      Bos sp.
XX
XX      PN      WO200149107-A1.
XX
XX      PD      12-JUL-2001.
XX
XX      PF      22-DEC-2000; 2000WO-CB004991.
XX
XX      PR      30-DEC-1999; 99GB-00030825.
XX
XX      PA      (SYNA-) SYNAPTICA LTD.
XX
XX      PI      Greenfield SA, Rawlins JNP, Deacon RMJ;
XX
XX      DR      WPI; 2001-441761/47.
XX
XX      PT      Providing animal model for Alzheimer's disease comprises introducing
PT      peptide fragment from close to C-terminus of acetylcholine esterase which
PT      causes cellular degeneration and impairment of testable brain function.
XX
XX      PS      Disclosure; Fig 1; 44pp; English.
XX
XX      CC      The sequence represents the amino acid sequence of a biologically active
CC      fragment of bovine acetylcholinesterase (AChE). The peptide is used in a
CC      method of providing an animal model for a neurodegenerative disease. This
CC      involves introducing the peptide fragment, from close to the C-terminus
CC      of AChE, or an active variant of the peptide, into one or more sites in
CC      the brain of a non-human animal, whereby the peptide causes cellular
CC      degeneration and leads to impairment of testable brain function that is
CC      indicative of a neurological disorder in a human. The animal model is
CC      useful for testing an agent for biological activity in a
CC      neurodegenerative disorder which involves administering the agent to a
CC      model for Alzheimer's disease and determining whether the agent will
CC      inhibit, prevent or decrease impairment of the testable brain function
CC      (cognitive function) and/or cause improvement or deterioration of
CC      cellular damage in the brain. The animal models are also useful as a
CC      model for Parkinson's disease, motor neuron disease and prion-related
CC      diseases and thus for testing reagents to assess their potential for
CC      treatment of Parkinson's disease. The AChE peptide causes considerable
CC      nervous system damage, which is an order of magnitude greater than that
CC      of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
CC      be identified using simple behavioral tests known to be affected by
CC      hippocampal dysfunction
XX
SQ      Sequence 53 AA;
      Query Match      100.0%; Score 87; DB 4; Length 53;
      Best Local Similarity 100.0%; Pred. No. 1.1e-05;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEFHRWSSYVHWK 14
      |||||||
Db      25 AEFHRWSSYVHWK 38

RESULT 18
AAG65953
ID      AAG65953 standard; protein; 53 AA.
XX
XX      AC      AAG65953;
XX
XX      DT      11-FEB-2002 (first entry)
XX
XX      DE      Bovine acetylcholinesterase (AChE) partial sequence.
XX
XX      KW      Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
KW      antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
KW      Parkinson's disease; motor neuron disease.
XX
XX      OS      Bos sp.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      Peptide      25..38
XX      FT      /note= "synaptica peptide"
XX
XX      PN      WO200173446-A1.
XX
XX      PD      04-OCT-2001.
XX
XX      PF      29-MAR-2001; 2001WO-GB001401.
XX
XX      PR      29-MAR-2000; 2000GB-00007630.
XX      PR      15-DEC-2000; 2000GB-00030660.
XX
XX      PA      (SYNA-) SYNAPTICA LTD.
XX
XX      PI      Westwell M, Greenfield SA;
XX
XX      DR      WPI; 2001-639255/73.
XX
XX      PT      Use of alpha 7 nicotinic receptor or its functional analog to determine
PT      if a compound is capable of acting as functional analog or antagonist of
PT      acetylcholinesterase polypeptide for treating neurological disorders.
XX
XX      PS      Disclosure; Fig 1; 45pp; English.
XX
XX      CC      The invention relates to the use of an alpha 7 nicotinic receptor (I) or
XX      its functional analog to determine whether a compound is capable of
XX      acting as a functional analog or antagonist of an acetylcholinesterase
XX      (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
XX      native alpha 7 nicotinic receptor in its normal membrane environment, it
XX      is identified by means of inhibition by a blocker of (I). Methods for
XX      identifying a functional analog or antagonist of the synaptica peptide
XX      are also provided. The identified functional analog or antagonist is
XX      useful for the preparation of a medicament for treatment of a
XX      neurological disorder associated with non-enzymatic action of AChE, where
XX      the neurological disorder is Alzheimer's disease, Parkinson's disease or
XX      motor neuron disease. It is useful for inhibiting or preventing non-
XX      enzymatic activity of the synaptica peptide in vivo. The present sequence
XX      represents the partial sequence of bovine AChE polypeptide containing the
XX      synaptica peptide fragment
XX
SQ      Sequence 53 AA;
      Query Match      100.0%; Score 87; DB 4; Length 53;
      Best Local Similarity 100.0%; Pred. No. 1.1e-05;
      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AEFHRWSSYVHWK 14
      |||||||
Db      25 AEFHRWSSYVHWK 38

RESULT 19
AAU04703

```


ID AAU04703 standard; peptide; 54 AA.
 AC AAU04703;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Rabbit acetylcholinesterase (AChE) fragment.
 XX
 KW Acetylcholinesterase; AChE; neurodegenerative disease; brain;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;
 KW motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
 KW hippocampal dysfunction; rabbit.
 XX
 OS Oryctolagus sp.
 XX
 FN WO200149107-A1.
 XX
 PD 12-JUL-2001.
 XX
 XX 22-DEC-2000; 2000WO-GB004991.
 PF
 XX 30-DEC-1999; 99GB-00030825.
 PR
 XX (SYNA-) SYNAPTICA LTD.
 PA
 XX Greenfield SA, Rawlins JNP, Deacon RMJ;
 PI WPI; 2001-441761/47.
 XX
 DR Providing animal model for Alzheimer's disease comprises introducing
 PT peptide fragment from close to C-terminus of acetylcholine esterase which
 PT causes cellular degeneration and impairment of testable brain function.
 XX
 PS Disclosure; Fig 1; 44pp; English.
 XX
 CC The sequence represents the amino acid sequence of a biologically active
 CC fragment of rabbit acetylcholinesterase (AChE). The peptide is used in a
 CC method of providing an animal model for a neurodegenerative disease. This
 CC involves introducing the peptide fragment, from close to the C-terminus
 CC of AChE, or an active variant of the peptide, into one or more sites in
 CC the brain of a non-human animal, whereby the peptide causes cellular
 CC degeneration and leads to impairment of testable brain function that is
 CC indicative of a neurological disorder in a human. The animal model is
 CC useful for testing an agent for biological activity in a
 CC neurodegenerative disorder which involves administering the agent to a
 CC model for Alzheimer's disease and determining whether the agent will
 CC inhibit, prevent or decrease impairment of the testable brain function
 CC (cognitive function) and/or cause improvement or deterioration of
 CC cellular damage in the brain. The animal models are also useful as a
 CC model for Parkinson's disease, motor neuron disease and prion-related
 CC diseases and thus for testing reagents to assess their potential for
 CC treatment of Parkinson's disease. The AChE peptide causes considerable
 CC nervous system damage, which is an order of magnitude greater than that
 CC of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
 CC be identified using simple behavioral tests known to be affected by
 CC hippocampal dysfunction
 XX
 SQ Sequence 54 AA;
 Query Match 100.0%; Score 87; DB 4; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 26 AEFHRWSSYVHWK 39
 RESULT 20
 AAG65950
 ID AAG65950 standard; protein; 54 AA.
 XX
 AC AAG65950;
 XX
 11-FEB-2002 (first entry)
 XX
 DE Rabbit acetylcholinesterase (AChE) partial sequence.
 XX
 KW Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptic;
 KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
 KW Parkinson's disease; motor neuron disease.
 XX
 OS Oryctolagus cuniculus.
 XX
 FN WO200173446-A1.
 XX
 PD 04-OCT-2001.
 XX
 XX 29-MAR-2001; 2001WO-GB001401.
 PF
 XX 29-MAR-2000; 2000GB-00007630.
 PR
 XX 15-DEC-2000; 2000GB-00030660.
 PR
 XX (SYNA-) SYNAPTICA LTD.
 PA
 XX Westwell M, Greenfield SA;
 PI WPI; 2001-639255/73.
 XX
 DR Use of alpha 7 nicotinic receptor or its functional analog to determine
 PT if a compound is capable of acting as functional analog or antagonist of
 PT acetylcholinesterase polypeptide for treating neurological disorders.
 XX
 PS Disclosure; Fig 1; 45pp; English.
 XX
 CC The invention relates to the use of an alpha 7 nicotinic receptor (I) or
 CC its functional analog to determine whether a compound is capable of
 CC acting as a functional analog or antagonist of an acetylcholinesterase
 CC (AChE) polypeptide fragment (synaptic peptide) on (I). If (I) is a
 CC native alpha 7 nicotinic receptor in its normal membrane environment, it
 CC is identified by means of inhibition by a blocker of (I). Methods for
 CC identifying a functional analog or antagonist of the synaptic peptide
 CC are also provided. The identified functional analog or antagonist is
 CC useful for the preparation of a medicament for treatment of a
 CC neurological disorder associated with non-enzymatic action of AChE, where
 CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
 CC motor neuron disease. It is useful for inhibiting or preventing non-
 CC enzymatic activity of the synaptic peptide in vivo. The present sequence
 CC represents the partial sequence of rabbit AChE polypeptide containing the
 CC synaptic peptide fragment
 XX
 SQ Sequence 54 AA;
 Query Match 100.0%; Score 87; DB 4; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 26 AEFHRWSSYVHWK 39
 RESULT 21
 AAB50037
 ID AAB50037 standard; protein; 67 AA.
 XX
 AC AAB50037;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Acetylcholinesterase protein #2 used in a yeast two-hybrid system.
 XX

KW ASP; haemostatic; acetylcholinesterase; AChE; cell growth; human;
KW cell differentiation; thrombocytopenia; post-irradiation condition;
KW post-chemotherapy condition; blood loss; stress-induced male infertility.
XX Homo sapiens.
XX WO200073427-A2.
XX PN
XX PD
XX PF 07-DEC-2000.
XX PF 31-MAY-2000; 2000WO-IL000311.
XX PR 31-MAY-1999; 99IL-00130224.
XX PR 02-SEP-1999; 99IL-00131707.
XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI
XX PI Soreq H, Eldor A, Deutch V, Grisaru D;
XX WPI; 2001-061523/07.
XX DR
XX PT New regulatory peptides having cell growth and cell differentiation
PT activity derived from the C-terminal region of acetylcholinesterase
PT useful in promoting growth, survival and differentiation of stem cells.
XX PS
XX PS Claim 8; Page 87; 133pp; English.
XX CC
CC The present invention relates to C-terminal peptides of
CC acetylcholinesterase (AChE) (see AAB50032-B50034). The peptides of the
CC present invention have cell growth and/or cell differentiation activity.
CC The peptides may be used in ex vivo or in vivo expansion of
CC haematopoietic stem cells and neural progenitors, and in the promotion of
CC megakaryocytic differentiation of hematopoietic stem cells. In addition,
CC the peptides may be used in for promoting expansion of committed neural
CC progenitors in a developing embryo, in cultured embryonic stem cells, and
CC embryoid bodies derived from them. The peptides may further be used in
CC the treatment of thrombocytopenia, post-irradiation conditions, post-
CC chemotherapy conditions, and conditions following massive blood loss, in
CC inducing synthesis of AChE mRNA, and in promoting formation of hematon
CC bodies. Antibodies directed against the peptides are useful for
CC diagnosing stress-induced male infertility. The present sequence is a C-
CC terminal AChE "synaptic" protein (ASP), which was used in a yeast two-
CC hybrid system, to screen for ARP binding partners
XX SQ
SQ Sequence 67 AA;
Query Match 100.0%; Score 87; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
Db 39 AEFHRWSSYVHWK 52
|||||
RESULT 22
ABG31332
ID ABG31332 standard; protein; 68 AA.
XX AC
XX AC ABG31332;
XX DT
XX DT 05-NOV-2002 (first entry)
XX DE
XX DE GFP-fused AChE variant expression construct, pGASP related protein.
KW Nervous system; drug assay; acetylcholinesterase; AChE; brain;
KW isoform variance; AChE blocker; muscarinic receptor; M1; M2;
KW pyridostigmine; muscarinic receptor blocker; scopolamine;
KW M1 receptor blocker; pirenzepine; anxiety; post-traumatic stress;
KW Alzheimer's disease; muscle malfunctioning; neurodegenerative disorder;
KW xenobiotic damage; panic; neuromuscular disorder; Parkinson's disease;
KW Huntington's chorea; muscle fatigue; multiple chemical sensitivity;
KW autism; multiple sclerosis; Sjogren's disease; GFP; pGASP;

KW green fluorescent protein.
XX OS
XX OS Unidentified.
XX PN
XX PN WO200240994-A2.
XX PD
XX PD 23-MAY-2002.
XX PF
XX PF 14-NOV-2001; 2001WO-IL001051.
XX PR
XX PR 14-NOV-2000; 2000US-0247970P.
XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI
XX PI Soreq H, Meshorer E, Sklan E, Shoham S;
XX XX WPI; 2002-490152/52.
XX XX
XX PT Evaluating effect of drugs on nervous system by comparing effect of drug
PT on acetylcholinesterase, AChE activity in brain of test animal following
PT challenge by AChE blocker and comparing it with control group.
XX PS
XX PS Example; Page 52; 114pp; English.
XX CC
CC The present invention relates to a method and system for evaluating an
CC effect on the nervous system of a test drug. The method comprises
CC comparing the effect of the drug on acetylcholinesterase (AChE) catalytic
CC activity or isoform variance in a brain of a test animal following a
CC challenge by an AChE blocker or a blocker of AChE and muscarinic
CC receptors M1 and M2 (e.g. pyridostigmine) and comparing this effect with
CC that of a known agent, preferably a non-selective muscarinic receptor
CC blocker (e.g. scopolamine) or a specific M1 receptor blocker (e.g.
CC pirenzepine). The method is useful for evaluating an effect on the
CC nervous system of a test drug, including drugs for the treatment of
CC anxiety conditions, post-traumatic stress, Alzheimer's disease, muscle
CC malfunctioning, neurodegenerative disorders, damage resulting from
CC exposure to xenobiotics, panic, neuromuscular disorders, Parkinson's
CC disease, Huntington's chorea, muscle fatigue, multiple chemical
CC sensitivity, autism, multiple sclerosis and Sjogren's disease. The
CC present sequence represents a protein described in relation to green
CC fluorescent protein (GFP)-fused AChE variant expression construct pGASP
CC in the examples of the present invention
XX SQ
SQ Sequence 68 AA;
Query Match 100.0%; Score 87; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
Db 40 AEFHRWSSYVHWK 53
|||||
RESULT 23
ADL90218
ID ADL90218 standard; protein; 348 AA.
XX AC
XX AC ADL90218;
XX DT
XX DT 17-JUN-2004 (first entry)
XX DE
XX DE Human enzyme, ENZM-28, SEQ ID 28.
XX KW
KW Cytostatic; Antiartherosclerotic; Anticonvulsant; Nootropic;
KW Neuroprotective; Cerebroprotective; Anti-HIV; Antiallergic;
KW Antiinflammatory; Thyromimetic; Gene therapy; human; enzyme;
KW cell proliferative disorder; cancer; atherosclerosis;
KW neurological disorder; epilepsy; Huntington's disease; stroke;
KW immune disorder; inflammatory disorder; AIDS; allergies;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW ENZM-28.
XX XX

PD 26-SEP-1990.
 XX
 PF 20-MAR-1990; 90EP-00105274.
 XX
 PR 21-MAR-1989; 89IL-00089703.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 XX
 XX Soreq H, Zakut H;
 PI
 XX WPI; 1990-291865/39.
 DR N-PSDB; AAQ05999.
 XX
 CC Human acetylcholinesterase genetic molecules, peptide(s) - used for
 PT organo-phosphorus poisoning, diagnosis or ovarian carcinoma(s) and haemo-
 PT cytopositic, etc. disorders.
 XX
 PS Disclosure; Fig 1c; 47pp; English.
 XX
 CC Gene product is useful as an active pharmacological component for the
 CC prophylaxis and treatment of organophosphorous poisoning, and post-
 CC surgical apnea due to succinylcholine administration. cDNA probe to the
 CC sequence may be used in diagnosis of various leukaemias, abnormal
 CC megakaryocytopoiesis and ovarian carcinomas. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 500 AA;
 Query Match 100.0%; Score 87; DB 2; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYMVHWK 14
 |||||
 DB 472 AEFHRWSSYMVHWK 485
 |||||
 RESULT 26
 ABR38991
 ID ABR38991 standard; protein; 526 AA.
 XX
 AC ABR38991;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human acetylcholinesterase isomer protein #SEQ ID 2.
 XX
 KW Human; acetylcholinesterase; enzyme; AR-ACHE; cell withering.
 XX
 OS Homo sapiens.
 XX
 PN CN1376798-A.
 XX
 PD 30-OCT-2002.
 XX
 PF 23-MAR-2001; 2001CN-00105781.
 XX
 PR 23-MAR-2001; 2001CN-00105781.
 XX
 PA (SHAN-) SHANGHAI CELL BIOLOGY INST CHINESE ACAD.
 XX
 PI Zhang X, Yang L, He H;
 XX
 DR WPI; 2003-211570/21.
 DR N-PSDB; ACC47509.
 XX
 CC Human acetylcholinesterase isomer protein (AR-ACHE) and its gene coding
 PT sequence.
 PT
 XX Claim 3; Page 9 (disclosure); 19pp; Chinese.
 PS
 XX The invention relates to a novel human acetylcholinesterase isomer
 CC protein (AR-ACHE) expressed when human tissue cells wither. Also

CC disclosed is the gene sequence encoding the protein. The cDNA is 1936 bp
 CC in length and the protein is composed of 526 amino acid residues. The
 CC process for preparing the protein and nucleic acid sequence, the process
 CC for detecting the AR-ACHE nucleic acid sequence and polypeptide in a
 CC sample, and the process for promoting or inhibiting cell withering are
 CC also disclosed. The current sequence represents the human
 CC acetylcholinesterase isomer protein amino acid sequence
 XX
 SQ Sequence 526 AA;
 Query Match 100.0%; Score 87; DB 6; Length 526;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYMVHWK 14
 |||||
 DB 498 AEFHRWSSYMVHWK 511
 |||||
 RESULT 27
 ADR21588
 ID ADR21588 standard; protein; 526 AA.
 XX
 AC ADR21588;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human enzyme ENZM-9 protein SEQ ID NO:9.
 XX
 KW human; enzyme; ENZM-9; immunosuppressive; antiinflammatory;
 KW antimicrobial; neuroprotective; cardiovascular; ophthalmological;
 KW gynaecological; cytostatic; gene therapy; immune deficiency;
 KW autoimmune disorder; inflammatory disorder; infectious disorder;
 KW neurological disorder; cardiovascular disorder; eye disorder;
 KW metabolic disorder; reproductive disorder; cell proliferative disorder;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004072267-A2.
 XX
 PD 26-AUG-2004.
 XX
 PF 12-FEB-2004; 2004WO-US004280.
 XX
 PR 12-FEB-2003; 2003US-0447246P.
 PR 21-FEB-2003; 2003US-0449087P.
 PR 26-FEB-2003; 2003US-0450622P.
 PR 21-MAR-2003; 2003US-0456704P.
 PR 15-APR-2003; 2003US-0463194P.
 PR 09-MAY-2003; 2003US-0469358P.
 PR 02-JUN-2003; 2003US-0475532P.
 PR 04-JUN-2003; 2003US-0476278P.
 PR 27-JUN-2003; 2003US-0483395P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Kable AE, Yue H, Baughn MR, Tribouley CM, Ring HZ, Tran UK;
 PI Emerling BM, Rankumar J, Hafalia AJA, Swarnakar A, Lee SY;
 PI Chawla NK, Gietzen KJ, Marguis JP, Elliott VS, Becha SD, Favero KD;
 PI Wang JT, Naidu S, Hawkins PR, Jin P, Chien D;
 XX
 DR WPI; 2004-625866/60.
 DR N-PSDB; ADR21627.
 XX
 CC New enzymes, useful for diagnosing, treating, or preventing autoimmune,
 PT inflammatory, infectious, neurological, cardiovascular, eye, metabolic,
 PT reproductive, or cell proliferative disorders including cancer.
 XX
 PS Claim 1; SEQ ID NO 9; 305pp; English.
 XX
 CC The present sequence represents a human enzyme designated ENZM-9. Human
 CC ENZM sequences have immunosuppressive, antiinflammatory, antimicrobial,

CC neuroprotective, cardiovascular, ophthalmological, gynaecological and
 CC cytoskeletal activities, and can be used in gene therapy. The human ENZM
 CC polypeptides, polynucleotides, compositions, and methods of the present
 CC invention can be used for diagnosing, treating, or preventing immune
 CC deficiencies, or autoimmune, inflammatory, infectious, neurological,
 CC cardiovascular, eye, metabolic, reproductive, or cell proliferative
 CC disorders including cancer (e.g. breast, lung, colon, or ovarian cancer).
 XX
 XX SQ Sequence 526 AA;

Query Match 100.0%; Score 87; DB 8; Length 526;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 |||||
 Db 498 AEFHRWSSYVHWK 511

RESULT 28

AAG80773
 ID AAG80773 standard; protein; 583 AA.

AC AAG80773;

XX 19-APR-2002 (first entry)

XX AChE protein fragment #2.

XX AChE; acetylcholinesterase; ds.

XX Unidentified.

XX KR98077837-A.

XX 16-NOV-1998.

XX 23-APR-1997; 97KR-00015104.

XX 23-APR-1997; 97KR-00015104.

XX (GLDS) LG CHEM LTD.

XX Lee JH, Kim CH, Cho JM, Yoon HS;

XX WPI; 2000-035682/03.

XX N-PSDB; ABA97180.

XX Novel acetylcholinesterase gene and process for preparing

PT acetylcholinesterase from E-coli using the same.

XX Disclosure; Page 17-19; 23pp; Korean.

XX This sequence represents the encoding nucleic fragment from
 CC acetylcholinesterase acid which is described in the disclosure of the
 CC invention

XX SQ Sequence 583 AA;

Query Match 100.0%; Score 87; DB 3; Length 583;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 |||||
 Db 555 AEFHRWSSYVHWK 568

RESULT 29

AAG80772

ID AAG80772 standard; protein; 584 AA.

XX AAG80772;

XX
 DT
 XX
 DE
 XX
 KW
 XX
 OS
 XX
 FH

19-APR-2002 (first entry)

AChE protein.

AChE; acetylcholinesterase.

Unidentified.

Key Location/Qualifiers

Misc-difference 119 /note= "Encoded by TTC"

Misc-difference 122 /note= "Encoded by GGT"

Misc-difference 123 /note= "Encoded by GGC"

Misc-difference 160 /note= "Encoded by CYG"

Misc-difference 203 /note= "Encoded by GAG"

Misc-difference 244 /note= "Encoded by GAG"

Misc-difference 269 /note= "Encoded by GAG"

Misc-difference 335 /note= "Encoded by GAG"

Misc-difference 336 /note= "Encoded by GAG"

Misc-difference 364 /note= "Encoded by GGT"

Misc-difference 365 /note= "Encoded by GCG"

Misc-difference 406 /note= "Encoded by CAA"

Misc-difference 407 /note= "Encoded by CAT"

KR98077837-A.

16-NOV-1998.

23-APR-1997; 97KR-00015104.

23-APR-1997; 97KR-00015104.

(GLDS) LG CHEM LTD.

Lee JH, Kim CH, Cho JM, Yoon HS;

WPI; 2000-035682/03.

N-PSDB; ABA97179.

Novel acetylcholinesterase gene and process for preparing

PT acetylcholinesterase from E-coli using the same.

XX Disclosure; Page 13-15; 23pp; Korean.

This sequence represents a the acetylcholinesterase acid protein which is

described in the disclosure of the invention

XX SQ Sequence 584 AA;

Query Match 100.0%; Score 87; DB 3; Length 584;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14

|||||

Db 556 AEFHRWSSYVHWK 569

RESULT 30

AAR06989

ID AAR06989 standard; protein; 613 AA.
 XX AAR06989;
 AC
 XX 25-MAR-2003 (revised)
 DT 16-JAN-1991 (first entry)
 XX
 DE Human acetylcholinesterase (hAChE) primary transcript.
 XX
 KW Organophosphorous poisoning; OP; cancer; leukaemia; megakaryocytopoiesis;
 KW ovarian cancer.
 XX
 OS Homo sapiens.
 XX
 PN EP388906-A.
 XX
 PD 26-SEP-1990.
 XX
 PF 20-MAR-1990; 90EP-00105274.
 XX
 PR 21-MAR-1989; 89IL-00089703.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Soreq H, Zakut H;
 XX
 DR WPI; 1990-291865/39.
 DR N-PSDB; AAQ05998.
 XX
 PT Human acetylcholinesterase genetic molecules, peptide(s) - used for
 PT organo-phosphorus poisoning, diagnosis or ovarian carcinoma(s) and haemo-
 PT cytopoietic, etc. disorders.
 XX
 PS Claim 5; Page 25; 47pp; English.
 XX
 CC Gene product is useful as an active pharmacological component for the
 CC prophylaxis and treatment of organophosphorous poisoning, and post-
 CC surgical apnea due to succinylcholine administration. cDNA probe to the
 CC sequence may be used in diagnosis of various leukaemias, abnormal
 CC megakaryocytopoiesis and ovarian carcinomas. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 613 AA;
 Query Match 100.0%; Score 87; DB 2; Length 613;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVHWK 14
 ||||||||||||
 Db 585 AEFHRWSSYVHWK 598
 RESULT 31
 AAR80726
 ID AAR80726 standard; protein; 614 AA.
 XX
 AC AAR80726;
 XX
 DT 31-MAR-1996 (first entry)
 XX
 DE Human acetylcholinesterase (AChE) protein.
 XX
 KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7; chromosome-7q22;
 KW acetylcholine-hydrolyzing enzyme.
 XX
 OS Homo sapiens.
 XX
 PN W09523158-A1.
 XX
 PD 31-AUG-1995.
 XX
 PF 28-FEB-1995; 95WO-US002806.

XX 28-FEB-1994; 94US-00202755.
 PR 09-JAN-1995; 95US-00370156.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 PA (KOHN/) KOHN K I.
 XX
 PI Soreq H, Zakut H, Shani M;
 XX
 DR WPI; 1995-311499/40.
 DR N-PSDB; AAQ99002.
 XX
 PT Alternative forms of human acetyl cholinesterase (ChE) gene - expressed
 PT in transgenic animal assay system for evaluating anti-ChE activity of
 PT organo:phosphate(s), etc. or as model of ChE imbalance.
 XX
 PS Claim 3; Fig 1B; 55pp; English.
 XX
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at neuromuscular
 CC junctions where it serves a vital function in modulating cholinergic
 CC neurotransmission. Alternatively spliced forms of human AChE may be
 CC expressed in transgenic animals which are used in an assay system for
 CC determining the anti-ChE activity of organophosphates, carbamates, anti-
 CC ChE drugs, plant glycoalkaloids and snake venoms
 XX
 SQ Sequence 614 AA;
 Query Match 100.0%; Score 87; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVHWK 14
 ||||||||||||
 Db 586 AEFHRWSSYVHWK 599
 RESULT 32
 AAY49490
 ID AAY49490 standard; protein; 614 AA.
 XX
 AC AAY49490;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Human acetylcholinesterase (AChE) mutant.
 XX
 KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; Cat; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US6001625-A.
 XX
 PD 14-DEC-1999.
 XX
 PF 19-MAY-1995; 95US-00446100.
 XX
 PR 19-MAY-1995; 95US-00446100.
 XX
 PA (USSA) US SEC OF ARMY.
 XX
 PI Broomfield CA, Lockridge O, Millard CB;
 XX
 DR WPI; 2000-096137/08.
 XX
 PT Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 XX
 PS Disclosure; Col 13-14; 64pp; English.
 XX
 CC The invention provides a method of enhancing organophosphate detoxifying

CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 CC
 SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 |||||
 Db 586 AEFHRWSSYVHWK 599

RESULT 33
 AAY49489
 ID AAY49489 standard; protein; 614 AA.
 AC AAY49489;
 XX
 XX 27-MAR-2000 (first entry)
 DT
 DE Human wild-type acetylcholinesterase (AChE).

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA.

XX Homo sapiens.
 OS
 XX US6001625-A.
 PN
 XX 14-DEC-1999.
 PD
 XX 19-MAY-1995; 95US-00446100.
 PF
 XX 19-MAY-1995; 95US-00446100.
 PR
 XX (USSA) US SEC OF ARMY.

XX Broomfield CA, Lockridge O, Millard CB;
 PI
 XX WPI; 2000-096137/08.
 DR
 XX
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.

XX Disclosure; Col 11-14; 64pp; English.
 PS
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to

CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 CC
 SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 |||||
 Db 586 AEFHRWSSYVHWK 599

RESULT 34
 AAY49493
 ID AAY49493 standard; protein; 614 AA.
 AC AAY49493;
 XX

XX 27-MAR-2000 (first entry)
 DT
 DE Human acetylcholinesterase (AChE) mutant.

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.

XX Homo sapiens.
 OS
 XX Synthetic.
 XX US6001625-A.
 PN
 XX 14-DEC-1999.
 PD

XX 19-MAY-1995; 95US-00446100.
 PF
 XX 19-MAY-1995; 95US-00446100.
 PR
 XX (USSA) US SEC OF ARMY.

XX Broomfield CA, Lockridge O, Millard CB;
 PI
 XX WPI; 2000-096137/08.
 DR
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.

XX Disclosure; Col 15-16; 64pp; English.
 PS
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;

Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | | | | | | | |
Db 586 AEFHRWSSYVHWK 599

RESULT 35
AAY49492
ID AAY49492 standard; protein; 614 AA.
XX AC AAY49492;
XX XX
XX 27-MAR-2000 (first entry)
XX Human acetylcholinesterase (AChE) mutant.
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX US6001625-A.
XX 14-DEC-1999.
XX 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
XX (USSA) US SEC OF ARMY.
XX Broomfield CA, Lockridge O, Millard CB;
XX WPI; 2000-096137/08.
XX Enhancing the organophosphate detoxifying capabilities of esterases for
XX the treatment of organophosphate poisoning.
XX Disclosure; Col 13-16; 64pp; English.
XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE), that
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX Sequence 614 AA;
SQ Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | | | | | | | |
Db 586 AEFHRWSSYVHWK 599

RESULT 36
AAY49495
ID AAY49495 standard; protein; 614 AA.
XX AC AAY49495;
XX XX
XX 27-MAR-2000 (first entry)
XX Human acetylcholinesterase (AChE) mutant.
XX

AAY49491
ID AAY49491 standard; protein; 614 AA.
XX AC AAY49491;
XX 27-MAR-2000 (first entry)
XX Human acetylcholinesterase (AChE) mutant.
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX US6001625-A.
XX 14-DEC-1999.
XX 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
XX (USSA) US SEC OF ARMY.
XX Broomfield CA, Lockridge O, Millard CB;
XX WPI; 2000-096137/08.
XX Enhancing the organophosphate detoxifying capabilities of esterases for
XX the treatment of organophosphate poisoning.
XX Disclosure; Col 13-14; 64pp; English.
XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX Sequence 614 AA;
SQ Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | | | | | | | |
Db 586 AEFHRWSSYVHWK 599

RESULT 37
AAY49495
ID AAY49495 standard; protein; 614 AA.
XX AC AAY49495;
XX XX
XX 27-MAR-2000 (first entry)
XX Human acetylcholinesterase (AChE) mutant.
XX

KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN US6001625-A.
 XX
 XX 14-DEC-1999.
 XX
 XX 19-MAY-1995; 95US-00446100.
 XX
 XX 19-MAY-1995; 95US-00446100.
 XX
 XX (USSA) US SEC OF ARMY.
 XX
 XX Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 XX
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 XX
 XX Disclosure; Col 15-16; 64pp; English.
 XX
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CAE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 SQ Sequence 614 AA;
 Query Match 100.0%; Score 87; DB 3; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVHWK 14
 | | | | | | | | | | | | | |
 DB 586 AEFHRWSSYVHWK 599
 RESULT 38
 AAY49494
 ID AAY49494 standard; protein; 614 AA.
 XX
 AC AAY49494;
 XX
 XX 27-MAR-2000 (first entry)
 DT
 XX Human acetylcholinesterase (AChE) mutant.
 DE
 XX
 KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US6001625-A.
 FN

PD 14-DEC-1999.
 XX
 XX 19-MAY-1995; 95US-00446100.
 XX
 XX 19-MAY-1995; 95US-00446100.
 XX
 XX (USSA) US SEC OF ARMY.
 XX
 XX Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 XX
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 XX
 XX Disclosure; Col 15-16; 64pp; English.
 XX
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CAE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 SQ Sequence 614 AA;
 Query Match 100.0%; Score 87; DB 3; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVHWK 14
 | | | | | | | | | | | | | |
 DB 586 AEFHRWSSYVHWK 599
 RESULT 39
 AAU11231
 ID AAU11231 standard; protein; 614 AA.
 XX
 AC AAU11231;
 XX
 XX 26-FEB-2002 (first entry)
 DT
 XX Human acetylcholinesterase, AChE.
 DE
 XX
 KW Human; AChE; acetylcholinesterase; polymorphic variant; haplotyping;
 KW genotyping; neurological disease; Parkinson's disease;
 KW Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
 XX
 OS Homo sapiens.
 XX
 XX WO200179219-A2.
 FN
 XX
 XX 25-OCT-2001.
 PD
 XX
 XX 11-APR-2001; 2001WO-US011853.
 PF
 XX
 XX 14-APR-2000; 2000US-0197173P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (KAZE/) KAZEMI A.
 PA
 XX Bentivegna SC, Chew A, Choi JY, Koshy B;

XX WPI; 2002-055248/07.
 DR N-PSDB; AAS17492, AAS17493.
 XX
 XX New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
 PT useful in expressing ACHE protein for use in screening for candidate
 PT drugs to treat diseases related to ACHE activity, e.g. neurological
 PT diseases or cancer.
 XX
 XX Claim 29; Fig 2; 79pp; English.
 PS
 XX The invention relates to a polynucleotide comprising a polymorphic
 CC variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
 CC complement, the variant comprising an ACHE isogene defined by a haplotype
 CC selected from haplotypes 1-20 listed in the specification. Also included
 CC are methods for haplotyping and genotyping the ACHE gene of an
 CC individual, a method for predicting a haplotype pair for the ACHE gene of
 CC an individual, a method for identifying an association between a trait
 CC and at least one haplotype or haplotype pair of ACHE gene, recombinant
 CC nonhuman organisms transformed or transfected with the polynucleotide
 CC where the organism expresses ACHE protein encoded by the first nucleotide
 CC sequence or encoded by the polymorphic variant sequence, an isolated
 CC antibody specific for and immunoreactive with ACHE, a method of screening
 CC for drugs targeting the polypeptide contacting ACHE polymorphic variant
 CC with a candidate agent and assaying for binding activity, a computer
 CC system for storing and analysing polymorphism data for ACHE gene and a
 CC genome anthology for ACHE gene which comprises ACHE isogenes defined by
 CC haplotypes 1-20 given in the specification. The Polymorphisms are useful
 CC for studying the biological function of ACHE as well as in identifying
 CC drugs targeting this protein for the treatment of disorder related to its
 CC abnormal expression or function. The polymorphic variants may also be
 CC used in screening for compounds targeting ACHE to treat a specific
 CC condition or disease predicted to be associated with ACHE activity e.g.
 CC neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
 CC cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
 CC 7q22. The present sequence is the ACHE protein
 XX
 SQ Sequence 614 AA;
 Query Match 100.0%; Score 87; DB 5; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVMHWK 14
 |||||
 DB 586 AEFHRWSSYVMHWK 599
 |||||
 RESULT 40
 AAU11232
 ID AAU11232 standard; protein; 614 AA.
 XX
 AC AAU11232;
 XX
 XX 26-FEB-2002 (first entry)
 DT
 DE Human acetylcholinesterase, ACHE variant #1.
 XX
 XX Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
 KW genotyping; neurological disease; Parkinson's disease;
 KW Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 34
 FT /note= "Wild-type Arg substituted by Gln"
 XX
 PN WO200179219-A2.
 XX
 XX 25-OCT-2001.
 PD
 XX 11-APR-2001; 2001WO-US011853.

XX 14-APR-2000; 2000US-0197173P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (KAZE/) KAZEMI A.
 XX
 XX Bentivegna SC, Chew A, Choi JY, Koshy B;
 FI WPI; 2002-055248/07.
 XX
 XX New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
 PT useful in expressing ACHE protein for use in screening for candidate
 PT drugs to treat diseases related to ACHE activity, e.g. neurological
 PT diseases or cancer.
 XX
 XX Claim 29; Page; 79pp; English.
 PS
 XX The invention relates to a polynucleotide comprising a polymorphic
 CC variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
 CC complement, the variant comprising an ACHE isogene defined by a haplotype
 CC selected from haplotypes 1-20 listed in the specification. Also included
 CC are methods for haplotyping and genotyping the ACHE gene of an
 CC individual, a method for predicting a haplotype pair for the ACHE gene of
 CC an individual, a method for identifying an association between a trait
 CC and at least one haplotype or haplotype pair of ACHE gene, recombinant
 CC nonhuman organisms transformed or transfected with the polynucleotide
 CC where the organism expresses ACHE protein encoded by the first nucleotide
 CC sequence or encoded by the polymorphic variant sequence, an isolated
 CC antibody specific for and immunoreactive with ACHE, a method of screening
 CC for drugs targeting the polypeptide contacting ACHE polymorphic variant
 CC with a candidate agent and assaying for binding activity, a computer
 CC system for storing and analysing polymorphism data for ACHE gene and a
 CC genome anthology for ACHE gene which comprises ACHE isogenes defined by
 CC haplotypes 1-20 given in the specification. The Polymorphisms are useful
 CC for studying the biological function of ACHE as well as in identifying
 CC drugs targeting this protein for the treatment of disorder related to its
 CC abnormal expression or function. The polymorphic variants may also be
 CC used in screening for compounds targeting ACHE to treat a specific
 CC condition or disease predicted to be associated with ACHE activity e.g.
 CC neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
 CC cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
 CC 7q22. The present sequence is an ACHE protein polymorphic variant. Note:
 CC the indexer from the ACHE sequence shown in figure 3 (AAU11231)
 XX
 SQ Sequence 614 AA;
 Query Match 100.0%; Score 87; DB 5; Length 614;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSYVMHWK 14
 |||||
 DB 586 AEFHRWSSYVMHWK 599
 |||||
 RESULT 41
 AAU11234
 ID AAU11234 standard; protein; 614 AA.
 XX
 AC AAU11234;
 XX
 XX 26-FEB-2002 (first entry)
 DT
 DE Human acetylcholinesterase, ACHE variant #3.
 XX
 XX Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
 KW genotyping; neurological disease; Parkinson's disease;
 KW Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH

```

FT Misc-difference 353
FX /note= "Wild-type His substituted by Asn"
FX
FX WO200179219-A2.
FX
FX 25-OCT-2001.
FX
FX 11-APR-2001; 2001WO-US011853.
FX
FX 14-APR-2000; 2000US-0197173P.
FX
FX (GENA-) GENAISSANCE PHARM INC.
FX (KAZE/) KAZEMI A.
FX
FX Bentivegna SC, Chew A, Choi JY, Koshiy B;
FX
FX WPI; 2002-055248/07.
FX
FX New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
FX useful in expressing ACHE protein for use in screening for candidate
FX drugs to treat diseases related to ACHE activity, e.g. neurological
FX diseases or cancer.
FX
FX Claim 29; Page; 79pp; English.
FX
FX The invention relates to a polynucleotide comprising a polymorphic
FX variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
FX complement, the variant comprising an ACHE isogene defined by a haplotype
FX selected from haplotypes 1-20 listed in the specification. Also included
FX are methods for haplotyping and genotyping the ACHE gene of an
FX individual, a method for predicting a haplotype pair for the ACHE gene of an
FX individual, a method for identifying an association between a trait
FX and at least one haplotype or haplotype pair of ACHE gene, recombinant
FX nonhuman organisms transformed or transfected with the polynucleotide
FX where the organism expresses ACHE protein encoded by the first nucleotide
FX sequence or encoded by the polymorphic variant sequence, an isolated
FX antibody specific for and immunoreactive with ACHE, a method of screening
FX for drugs targeting the polypeptide contacting ACHE polymorphic variant
FX with a candidate agent and assaying for binding activity, a computer
FX system for storing and analysing polymorphism data for ACHE gene and a
FX genome anthology for ACHE gene which comprises ACHE isogenes defined by
FX haplotypes 1-20 given in the specification. The polymorphisms are useful
FX for studying the biological function of ACHE as well as in identifying
FX drugs targeting this protein for the treatment of disorder related to its
FX abnormal expression or function. The polymorphic variants may also be
FX used in screening for compounds targeting ACHE to treat a specific
FX neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
FX cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
FX 7q22. The present sequence is an ACHE protein polymorphic variant. Note:
FX The present sequence is not shown in the specification but was created by
FX the indexer from the ACHE sequence shown in figure 3 (AAU11231)
FX
FX Sequence 614 AA;
FX
FX Query Match 100.0%; Score 87; DB 5; Length 614;
FX Best Local Similarity 100.0%; Pred. No. 0.00015;
FX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FX
FX Qy 1 AEFHRWSSYVHWK 14
FX | | | | | | | | | |
FX 586 AEFHRWSSYVHWK 599
FX
FX RESULT 42
FX AAU11233
FX ID AAU11233 standard; protein; 614 AA.
FX
FX AC AAU11233;
FX
FX DT 26-FEB-2002 (first entry)
FX
FX DE Human acetylcholinesterase, ACHE variant #2.
Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
genotyping; neurological disease; Parkinson's disease;
Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
Homo sapiens.
Key Location/Qualifiers
Misc-difference 280
/ note= "Wild-type Thr substituted by Ala"
WO200179219-A2.
25-OCT-2001.
11-APR-2001; 2001WO-US011853.
14-APR-2000; 2000US-0197173P.
(GENA-) GENAISSANCE PHARM INC.
(KAZE/) KAZEMI A.
Bentivegna SC, Chew A, Choi JY, Koshiy B;
WPI; 2002-055248/07.
New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
useful in expressing ACHE protein for use in screening for candidate
drugs to treat diseases related to ACHE activity, e.g. neurological
diseases or cancer.
Claim 29; Page; 79pp; English.
The invention relates to a polynucleotide comprising a polymorphic
variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
complement, the variant comprising an ACHE isogene defined by a haplotype
selected from haplotypes 1-20 listed in the specification. Also included
are methods for haplotyping and genotyping the ACHE gene of an
individual, a method for predicting a haplotype pair for the ACHE gene of an
individual, a method for identifying an association between a trait
and at least one haplotype or haplotype pair of ACHE gene, recombinant
nonhuman organisms transformed or transfected with the polynucleotide
where the organism expresses ACHE protein encoded by the first nucleotide
sequence or encoded by the polymorphic variant sequence, an isolated
antibody specific for and immunoreactive with ACHE, a method of screening
for drugs targeting the polypeptide contacting ACHE polymorphic variant
with a candidate agent and assaying for binding activity, a computer
system for storing and analysing polymorphism data for ACHE gene and a
genome anthology for ACHE gene which comprises ACHE isogenes defined by
haplotypes 1-20 given in the specification. The polymorphisms are useful
for studying the biological function of ACHE as well as in identifying
drugs targeting this protein for the treatment of disorder related to its
abnormal expression or function. The polymorphic variants may also be
used in screening for compounds targeting ACHE to treat a specific
neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
7q22. The present sequence is an ACHE protein polymorphic variant. Note:
The present sequence is not shown in the specification but was created by
the indexer from the ACHE sequence shown in figure 3 (AAU11231)
Sequence 614 AA;
Query Match 100.0%; Score 87; DB 5; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AEFHRWSSYVHWK 14
| | | | | | | | | |
586 AEFHRWSSYVHWK 599
RESULT 42
AAU11233
ID AAU11233 standard; protein; 614 AA.
AC AAU11233;
DT 26-FEB-2002 (first entry)
DE Human acetylcholinesterase, ACHE variant #2.
```

ABP59222
ID ABP59222 standard; protein; 614 AA.
XX
AC ABP59222;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human drug metabolising enzyme, DME-13, SEQ ID 13.
XX
KW Human; drug metabolising enzyme; anti-HIV; antiallergic;
KW antiinflammatory; antianaemic; thrombolytic; antilipaemic; antidiarrheic;
KW antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid;
KW cycostatic; hepatotropic; virucide; dermatological; antidiabetic;
KW nephrotropic; antigout; neuroprotective; thyromimetic; osteopathic;
KW antiarthritic; antipoxiatic; uropathic; ophthalmological; antirheumatic;
KW haemostatic; gene therapy; cell proliferative disorder; cancer;
KW developmental disorder; endocrine disorder; eye disorder;
KW metabolic disorder; gastrointestinal disorder; liver disorder;
KW autoimmune disorder; inflammatory disorder; DME-13.
XX
OS Homo sapiens.
XX
FN WO2003004608-A2.
XX
PD 16-JAN-2003.
XX
PF 05-JUL-2002; 2002WO-US021105.
XX
PR 06-JUL-2001; 2001US-0303745P.
PR 13-JUL-2001; 2001US-0303402P.
PR 27-JUL-2001; 2001US-0308158P.
PR 14-SEP-2001; 2001US-0322127P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Griffin JA, Ramkumar J, Emerling BM, Richardson TW, Li JX;
PI Warren BA, Honchell CD, Baughn MR, Tang YT, Lee EA, Elliott VS;
PI Yue H, Lee S, Swarnakar A, Forsythe IJ, Sanjanwala MM, Yao MG;
PI Zebarjadian Y, Gervad AE, Becha SD, Burford N;
XX
DR WPI: 2003-221588/21.
DR N-PSDB; ABZ81313.
XX
PT New drug metabolizing enzymes (DME) useful for diagnosing, treating or
PT preventing diseases or conditions associated with aberrant DME
PT expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma,
PT hepatitis or osteoporosis.
XX
PS Claim 1; Page 168-169; 181pp; English.
XX
CC The present invention relates to novel human drug metabolising enzymes,
CC DME-1 to DME-13 (ABP592210-ABP59222) and their coding sequences (ABZ81301-
CC ABZ81313). The sequences are useful for diagnosing, treating or
CC preventing disorders associated with aberrant expression of DME,
CC particularly cell proliferative disorders (e.g. arteriosclerosis,
CC atherosclerosis, cirrhosis, paroxysmal nocturnal haemoglobinuria,
CC polycythaemia vera, psoriasis, primary thrombocytopenia or cancer),
CC developmental disorders (e.g. renal tubular acidosis, anaemia or mental
CC retardation), endocrine (e.g. osteoporosis, thrombosis, diabetes), eye
CC disorders (e.g. glaucoma, keratitis), metabolic (e.g. hyperlipidaemia,
CC cystic fibrosis), gastrointestinal disorders (e.g. gastroenteritis,
CC diarrhoea), liver disorders (e.g. hepatitis, Reye's syndrome), or
CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma,
CC autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC glomerulonephritis, Goodpasture's syndrome, gout, Graves disease,
CC Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis,
CC osteoarthritis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,
CC Sjogren's syndrome, uveitis). They are also useful in the assessing the
CC effects of exogenous compounds on the expression of nucleic acid and
CC amino acid sequences of DME. The polynucleotides encoding DME are useful
CC for creating transgenic animals to model human disease

Sequence 614 AA;

Query Match 100.0%; Score 87; DB 6; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
|||||
DB 586 AEFHRWSSYVHWK 599
RESULT 44
ABB99726
ID ABB99726 standard; protein; 614 AA.
XX
AC ABB99726;
XX
DT 24-MAR-2003 (first entry)
XX
DE Amino acid sequence of human acetylcholinesterase (YT blood group).
XX
KW G protein-coupled receptor; GPCR; single cell biosensor; arrestin;
KW GPCR ligand; muscarinic receptor; acetylcholinesterase; YT blood group.
XX
OS Homo sapiens.
XX
FN WO200299381-A2.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-2002; 2002WO-US017606.
XX
PR 05-JUN-2001; 2001US-0295945P.
PR 04-JUN-2002; 2002US-00161916.
XX
PA (UVDU-) UNIV DUKE.
XX
PI Barak LS, Shetzline MA, Oakley RH, Caron MG;
XX
DR WPI: 2003-140644/13.
DR N-PSDB; ABZ23128.
XX
PT Novel single cell biosensor, useful for detecting G protein-coupled
PT receptor ligand in a sample, comprises cell overexpressing arrestin and G
PT protein-coupled receptor.
XX
PS Disclosure; Fig 3E; 103pp; English.
XX
CC The present sequence represents human acetylcholinesterase (YT blood
CC group). Single cell biosensors of the invention which overexpress the
CC muscarinic receptor are used to detect acetylcholinesterase inhibition.
CC The muscarinic receptor is a G protein-coupled receptor (GPCR) that
CC translocates arrestins. The specification describes a single cell
CC biosensor comprising a cell which overexpresses arrestin and at least one
CC GPCR, where the GPCR, the arrestin or the cell is detectably labeled for
CC monitoring internalisation of the GPCR. The biosensor detects various
CC bioactive ligand species in the sample, as opposed to other antibody-
CC based methods, such as radioimmunoassay, which detects only the ligand
CC species with the reactive epitope. The biosensor is useful for detecting
CC a GPCR ligand in a test sample, for monitoring a GPCR ligand in a mammal,
CC for detecting a compound which modulates a GPCR ligand in a test sample,
CC for continuous screening of GPCR ligands in a test sample, and for
CC detecting a compound that modulates GPCR internalisation in a test
CC sample. It is useful for altering GPCR internalisation. It is also useful
CC for detecting an inhibitor of acetylcholinesterase in a test sample
XX
SQ Sequence 614 AA;
Query Match 100.0%; Score 87; DB 6; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
|||||

Db 586 AEFHRWSSYVHWK 599 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 45
ADE61695 ID ADE61695 standard; protein; 614 AA.
XX AC ADE61695;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein AAB24586, SEQ ID NO 7617.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; AAB24586.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX FT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 7; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;

THIS PAGE BLANK (USPIC)